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Sequence 16, Appl
Sequence 142, App
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                              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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No.
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Score 1100; DB 3; Length 1205; Pred. No. 1.8e-85;

20.9%;

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               842 KE-GKNMLILGALPNLMFLSLYHNSYLGEKLVFK---TG-AFPNLRTLVIFNLDQLREIR
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PatentIn Release #1.0, Version #1.30
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1170 ETAWEEEVQEARRKGGELKRKIREQLARNPNQPII 1204
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ADDRESSER: BROWDY AND NEIMARK
ATREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/930,996A FILING DATE: 09-DEC-1997 PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/US96/05272 FILING DATE: 15-APR.1996 PRIOR APPLICATION DATA: APPLICATION NUMBER: IL 113,373
                                                                                                                                                                                                                                                                 ; Sequence 8, Application US/08930996A; Patent No. 6100449
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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APPLICANT: ORI, Naomi
APPLICANT: PARAN, Ilan
APPLICANT: ZAMIR, Daniel
TITLE OF INVENTION: A GENE
TITLE OF INVENTION: LOCUS
TITLE OF INVENTION: SELECT
NUMBER OF SEQUENCES: 12
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APPLICANT: FLUHR,
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                                                                                                                                                                  KFYEQLPSELEINPSLEALRRMVTLGYNHLPSHLKPCFLYLSIFPEDFEIQRNRLVGRWI 455
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Patent No. 6479731

GENERAL InPORMATION:
APPLICANT: Valent, Barbara S.
APPLICANT: Bryan, Gregory
APPLICANT: Bryan, Gregory
TITLE OF INVENTION: A Pi-ta GENE CONFERRING DISEASE RESISTANCE TO F.
FILE REFERENCE: BB-1136
CURRENT APPLICATION NUMBER: US/09/336,946B
CURRENT APPLICATION NUMBER: 60/095229
PRIOR APPLICATION NUMBER: 60/095229
PRIOR FILING DATE: 1998-08-04
NUMBER OF SEQ ID NOS: 74
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-SIPKWTGKLNNLRILNI-----AVMQISQ------
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llarity 24.9%; Pred. No. 4.1e-49;
Conservative 164; Mismatches 366;
              97
; SOPTWARE: Microsoft Office 97; SEQ ID NO 2; LENGTH: 928; TYPE: PRT; YPPE: PRT; ORGANISM: Oryza sativa US-09-336-946B-2
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 262; Conserv
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489 RVGTAGKIKTCRIHDIIRDITVSISRQENF-VLLPMGDGSDLVQENTRHIAFHGSMSCKT 528 DVNCKNEVLSCVHHMVLNFIRCKSIEENFSITLDHSQTTVRHADKVRLSLHFSNAHDT 548GLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLEDVTFLITQK 588 TPLAGLRLSQVRSMAFFGQVKCMPSIADYRLLRVLILCFWADQEKTSY 595 DFDRIALLCHKYLSIGYSSSIYSLPRSIGKLQGLQTLNMSSTYIAALPSEISKLQCLHT	Db 694 LRIVIL-LDLLPHCHRYIFT	Application US/09336946B Application US/09336946B 6479731 SAWATION: Valent, Barbara S. Bryan, Gregory E. I. du Pont de Nemours and Company E. I. du Pont de Nemours and Company ENICE: BB-1136 ENCE: B	Query Match
	GENERAL INFORMATION: APPLICANT: Valent, Barbara APPLICANT: Valent, Barbara APPLICANT: Valent, Barbara APPLICANT: Bryan, Gregory TITLE OF INVENTION: Modification of a Plant Disease Resistance Gene TITLE OF INVENTION: Specificity CURRENT PAPLICATION NUMBER: US/09/993,170 CURRENT APPLICATION NUMBER: 60/248,335 PRIOR FILING DATE: 2000-11-14 NUMBER OF SEQ ID NOS: 60 SOFTWARE: Microsoft Office 97 SEQ ID NO 58 LENGTH: 928 TYPE: PRT CREALISM: Oryza sativa US-09-993-170-58 Query Match Best Local Similarity 24.9%; Pred: No. 4.1e-49; Matches 262; Conservative 164; Mismatches 366; Indels 261; Gaps 37;		Db 291 QHQSSDVWEVDRILETIRTHIQDKRYFIIIEDIWASSMWDIVSR-GLPDNN-SCSRILIT 348 Qy 314 TRNVDLAEKCATASLVYHLDFLQMNDAISLLIRKTNKNHEDMESNKOWQKNVERIVNKCG 373

AND PA

Daniel
A GENE FAMILY FROM THE 12 FUSARIUM RESISTANCE
A CENE TOMATO AND USE THEREOF FOR TRANSFORMATION
SELECTIVE BREEDING OF TOMATO AND RELATED PLANTS

ADDRESSEE: BROWDY AND NEIMARK STREET: 419 Seventh Street, N.W., Suite 300 CITY: Washington

NUMBER OF SEQUENCES: 1

APPLICANT: ZAMIR, DA TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:

SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

20004

COUNTRY:

APPLICATION NUMBER: US/08/930,996A FILING DATE: 09-DEC-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05272
FILING DATE: 15-APPL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 113,373

LENGTH: 1240 amino acids SEQUENCE CHARACTERISTICS:

amino acid

MOLECULE TYPE: protein

TOPOLOGY:

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Query Match 12.0%; Score 633; DB 3; Length 1240;
Best Local Similarity 24.7%; Pred. No. 3.8e-45;
Matches 247; Conservative 190; Mismatches 379; Indels 184;
                                                                                                                                                                                                                                                                                        FILING DATE: 13-APR-1995
INFORMATION FOR SEQ ID NO: 4
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US-08-930-996A-4
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                                 EDIRNOSARN------VDEA----ELVGFSDSKKRLLEMIDTNANDGP-AKVICV 191
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                                                                                             ---DLTSIPELLQLRYLKITGNITV-KLPEKIQGLQHLQTLEADARATAVL-LDIVHTQC
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                                                                                                                           LLHELQGKVVVQVHHLSEYLIEELKEKRYFVVLDDLWILHDWNWINEIAFPKNNKKGSRI
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KMISSMIARLRGELNRRRWIADEVTLFSARVKEAIRRQESYHLGRRTSSSRPREEVD-
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RLLEMIDTNANDGPA----KVICVVGMGGLGKTALSRKIFESEEDIRKNFPCNAWITVSQ 227 116 BIEDLIDRLLSEGASGKOLTVVPIVGMGGLGKTTLAKAVY-NDESVKOHFDLKAWFCVSE 234

172

114 -NLKSRVEEVSSRNTRYNLVEPIS-SGTEDDMDSYAEDIRNQSARNVDEAELVGFSDSKK 171

| : : | : : | : | ENKQASNPSVRDWILERDAVDSAENLIEEVNYBALRIKVEGGHQNPSETSNQQVSDEPP

63 ELLKVWAEQIRDLSYDIEDSLDEPKVHIESQTLFRQLVKLRERHRIAIRIH----

2 EIGLAVGGAFLSSALNVLFDRLAPNGDLLNMFRKHKDHVK-LLKKLKMTLRGIQIVLSDA

3 ETVLSMARSLVGSAISKAASAAANETSLLLGVEKDIWYIKDELKTMQAFLRAAEVMKKKD

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33 AYNAPRITKGLLQBIGSIDLVDDNLNQLQVK-------LKERLKEKKFLIVLDDVW 283 --ILHDWNWINBIAFPKNNKKGSRIVITTRNVDLAEKCATASLVYHLDFLQMNDAISLLL 345

SFHRIELLKOMIRQLLGPSSLDQLLHELQGKVVVQVHHLSEYLIEELKEKRYFVVLDDLW

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284 NDNYNEWDELRNVFV--QGDIGSKIIVTTRKDSVALMMGNEQI--SMGNLSTEASWSLFQ 339
                                                                                     GMTTKDVGESYPNELINRSMIQRSRVGTAGKIKTC-RIHDIIRDITVSISRQENFVLLPM 523
                                                                                                                                                                                                                                                                 454 DEIIQDLGNQFFLELSSRSLFERVPNPSEGNIKELFLMHDLVNDL-AQLASSKLCIRLEB 512
                                                                                                                                                                     LRDNDILPAL----MLSYNDLPAHLKRCPSFCAIFPKDYPFRKEQVIHLWIANGLV-PVE
                                                            RKTNKOHEDMESNKOMQKWVERIVNKCGRLPLAILTIGAVLATK-QVSEWEKFYEQLPSE
                                                                                                                                               LEINPSLEALRRMVTLGYNHLPSHLKPCFLYLSIPPEDFEIQRNRLVGRWIAEGFVRPKV
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                                                                                                                                             Sequence 4, Application US/08930996A Patent No. 6100449
                                                                                                                                                                              GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ESHED, YUVAI
APPLICANT: ORI, NAOMI
APPLICANT: PARAN, Ilan
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-08-930-996A-4

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993 NLQTL------IVSGCXYLVXLPKTFSXL------KNLXHFDMRXTPXLK 1030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EKFYEQLPSEL-----EINPSLEALRRMVTLGYNHLPSHLKPCFLYLSIFPEDFEIQR 447
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                                                                                                                                                                                                                                                                                      367 MAEIVLSAFLITVV---FEKLAXEALKKIVRSKRIESELKKLKETLDQIQDLLNDASQKEV
                                                                                                                                                                                                                                                                                                                                      61 KDELLKVWAEQIRDLSYDIEDSLDEFKVHI------ESQTLFRQLV-----KLRER
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                                                                                                                                                                                          Query Match 11.8%; Score 622.5; DB 3; Length 1402; Best Local Similarity 23.4%; Pred. No. 3.7e-44; Matches 245; Conservative 178; Mismatches 353; Indels 269;
                                                                                                                                          /note= "RLG1A amino acids'
LENGTH: 1402 amino acids
                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
                                                                                                                       LOCATION: 1..1402
; OTHER INFORMATION:
US-09-004-838-11
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                amino acid
                TYPE: amino
STRANDEDNESS:
                                                                                            NAME/KEY:
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                                                                                                                                                                                                                                                     DLGEAQNLYGSLSVVKLENVVDRREAVKPKMREKNHVEQLSLEWSESISA--DNSQTERD 746
                                                                                                                                                                                                                                                                                                                                                                           IETLECLDSISSPPPL--LRTLGLNGSLEEMPNWIEQLTHLKKFNLWSSKLKEGKNMLIL 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | || || || || || GQLPCLKFLSV--KGMHGIRVVTEE-FYGRLSSKKPFNC--LEKLEFEDMTEWKQWHALG 854
                  ---IFGDRPKSLA 568
                                                                                        HAVCPDQLRMLRVLDLEDVTFLITQKDFDRIALLCHLKYLSIGYSSSIYSLPRSIGKLQG 628
                                                                                                                         HNILP-TLRSLRALSLSH--YKMEELPNDLFIKLKLLRFLDIS-RTNIKRLPDSICVLYN 625
                                                                                                                                                          LQTLNMSSTYIAALPSEISKLQCLHTLRCIRELEPDNFSLNHPMKCITNTICLPKVFTPL 688
                                                                                                                                                                                                                               689 VSRDNRAKQIAEFHMATKSFWSESFGVKVPKGIGKLRDLQVLE----YVDIRRTSSRAIK 744
                                                                                                                                                                                                                                                                                                     ELGQLSKL-RKLAVI------TKGSTKEKCKILYAAIEKLSSLQSLYMNAALLSD 792
                                                                                                                                                                                          LETLLLSSCKLEELPLQMEKLINL-----RHLDISN--------
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Sequence 11, Application US/09004838
Patent No. 6350933
GENERAL INFORMATION:
APPLICANT: Michelmore, Richard W.
APPLICANT: Shen, Kathy
APPLICANT: Bhen, Kathy
APPLICANT: Procedures and Materials for
TITLE OF INVENTION: Procedures and Materials for
TITLE OF INVENTION: Conferring Pest Resistance in Plants
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GSSPQLEKIEISCCRLESGIIGIIHLPRLK-EISLEYKS 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDGSDLVQENTRHIAFHGSMSCKTGLD-----WSIIRSLA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSEE: Townsend and Townsend and Crew LLP
F: Two Embarcadero Center, Eighth Floor
San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   023070-078810US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/781,734
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,838
FILING DATE: 09-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 0230;
TELECOMMUNICATION INPORMATION:
TELEPAX: (415) 576-0200
TELEPAX: (415) 576-0300
INPORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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STREET: Tw
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S45 CKTGLDWSII	ALGENERALITY TRADOLKE THE BOOSE TO THE TOTAL T	RESULT 9 US-09-864-680A-3 ; Sequence 3, Application US/09864680A ; Patent No. 6762285 ; GENERAL INFORMATION: ; APPLICANT: Stackawicz, Brian J ; APPLICANT: Dalbeck, Douglas	; APPLICANT: Tai, Thomas H ; TITLE OF INVENTION: BB2 RESISTANCE GENB ; FILE REFERENCE: 42250/234021 (5830-4A) ; CURRENT APPLICATION NUMBER: US/09/864,680A ; CURRENT FILING DATE: 2001-05-24 ; PRIOR APPLICATION NUMBER: US 09/360,186 ; PRIOR APPLICATION NUMBER: US 60/093,957	; PRIOR FILING DATE: 1998-07-23 ; NUMBER OF SEQ ID NOS: 14 ; SEQ ID NO 3 ; LENGTH: 905 ; TYPE: PRT ; ORGANISM: Capsicum annuum US-09-864-680A-3	Query Match 11.7%; Score 615.5; DB 4; Length 905; Best Local Similarity 23.1%; Pred. No. 7.3e-44; Matches 232; Conservative 204; Mismatches 360; Indels 209; Gaps 39;	QY 42 KDELKTMQAFLRAAEVMKKKDELLKVWAEQIRDLSYDIEDSLDBFRVHIE 91 :E	QY 92 SQTLFRQLVKLRERHRIAIRIHNLKSRVEEVSERNTRYNLVEPISSGTEDDM 143 :::	Qy 144 DSYAEDIRNQSARNVDEAELVGFSDSKKRLLEMIDTNANDGPAKVICVVGMGGLGKTALS 203
Db 1086 VSKKVXXXXNWXXGXXIXCFPKWEHLKKKSSMKXCLIMVLXKKPX 1130	MUMBER OF SEQ ID NOS: 9 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 3 LENGTH: 905 TYPE: PRT ORGANISM: Capsicum annuum US-09-360-186-3	Query Match Best Local Similarity 23.1%; Pred. No. 7.3e-44; Matches 232; Conservative 204; Mismatches 360; Indels 209; Gaps 39; Qy 42 KDELKTWOAFLRAAEVMKKKDELLKVWAEQIRDLSYDIEDSLDEFKVHIE 91 31 REELCALREKVSSLEVYKKFEKNNYFGE-WITHER 99	SQTLFRQLVKLRERHRIAIRIHNLKSRVEEVSSRNTRYNLVEPISSGTEDDM	RKIFESEEDIRKNPPCNAMITVSQSFHRIELLKDMIROLLGPSSLDQLLHELQGKVVVQV ::::::	QY 324 ATASLVYHLDFLQMNDAISLLRKTNKNHEDMESNKNMQKMVERIVNKGGRLPLAILTIG 383 : : : : : : : : : : : : : :	OY 384 AVLATKQ-VSEWEKFYEQLESELEINPSLEALRRMYTLGYNHLPSHLKPCFLYLSIFPED 442	OY 443 PEIQRNRLVGRWIAEGFVRBKVGMTTKDVGESYFNELINRSMIORSRVGTAGKIKTC 499	Qy 500 RIHDIIRDITVSISRQENFVLLPMGDGSDLVQENTRHIAFHGSMS 544

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Sequence 2, Application US/08930996A

Patent No. 6100449

GENERAL INFORMATION:
RAPLICANT: ESHED, Yuval

APPLICANT: ESHED, Yuval

APPLICANT: PARAN, Ilan

APPLICANT: ZAMIR, Daniel

TITLE OF INVENTION: A GENE FAMILY PROM THE 12 FUSARIUM RESISTANCE

TITLE OF INVENTION: LOCUS OF TOMATO AND USE THEREOF FOR TRANSFORMATION AND TITLE OF INVENTION: SELECTIVE BREEDING OF TOWATO AND RELATED PLANTS

NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                     SDIPVKNLARSWAMAEGFL--KLENDLEGEVEKCLQELVDRCLVLVSKRSRDGT--KIRSC 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                     802 IVMGFNRLKILLI-KYSPLKFWKATNDNFPVLERLMIRSCKNLKEIPIEFADIHTLQLIE 860
                                                                                                    384 AVLATKQ-VSEWEKFYEQLPSELEINPSLEALRRMVTLGYNHLPSHLKPCFLYLSIFPED 442
                                                                                                                                                                                                                                                              FEIQRNRLVGRWIAEGFVRPKVGMTTKDVGESYFNELINRSMI---QRSRVGTAGKIKTC 499
                                                                                                                                                                                                                                                                                                                                       CKTGLDWSII-----QLRMLRVLDLE 585
                                                                                                                                                                                                                                                                                                                                                                                             | || ::: ::|:||:| CPYGLYRALLITPVNRQLRDHDNNNLLKRTHSVFSFHLEPLYYVLKSEVVHFKLLKVLELR 587
                                                                                                                                                                                                                                                                                                                                                                                                                                    586 DVTFLITQKDFD----RIALLCHLKYLSIGYSSSIYSLPRSIGKLQGLQT--LNMSSTYI 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            640 AALPSEISKLQCLHTLRCIRELEFDNFSLNHPMKCITNTICLPKVFTPLVSRDNRAKQIA 699
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                                                                                    264 HHLSEYLIEELKEKRYFVVLDDLWILHDWNWINEIAFPKNNKKGSRIVITTRNVDLAEKC 323
                                                                                                                                             324 ATASLVYHLDFLQMNDAISLLLRKTNKNHEDMESNKNMQKMVERIVNKCGRLPLAILTIG 383
                                                                                                                                                                      GVENFSLRMSFMDQDESWS-LFKSAAFSSEALP--YEFETVGKQIADECHGLPLTIVVVA 357
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----KVKN------NMVGRDDQRKQLLEDL-TRSYSGEPKVIPIVGMGGIGKTTLA 191
                           RKIFESEEDIRKNFPCNAMITVSQSFHRIELLKDMIRQLLGPSSLDQLLHELQGKVVVQV 263
                                             KEVY-NDESILCREDVHAMATISQQHNKKEILLGLLHSTIKMDDRVKMIGEAB-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TPSTSLVDDSGIFGRKNEIENLVGRLLSM-DTKRKN--LAVVPIVGMGGMGKTTLAKAVY 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KCATASLVYHLDFLQMNDAISLLLRKTNKNHEDMESNKNMQKMVERIVNKCGRLPLAILT 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 VKLRERHRIAIR---IHNLKSRVEEVSSRNTRYNLVEPISS-----GTEDDMDSYAEDIR 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43 DELKTMQAFLRAAEVMKKKDELLKVWAEQIR---DLSYDIEDSLDBFKVHIESQTLFRQL
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LMHDLVNDL-AQIASSNHCIRLEDNKGSHML-EQCRH-----MSYSIGQDGEFEKLKSL
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                                                                                                                                                    COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,996A
FILING DATE: 09-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 11.4%; Score 598.5; DB 3; Best Local Similarity 24.3%; Pred. No. 3.5e-42; Matches 237; Conservative 189; Mismatches 349;
                     3: BROWDY AND NEIMARK
419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/930,996A
FILING DATE: 09-DEC-1997
PRIOR APPLICATION DATE:
APPLICATION NUMBER: PCT/US96/05272
FILING DATE: 15-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 113,373
FILING DATE: 13-APR-1995
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 1220 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
CORRESPONDENCE ADDRESS
                     ADDRESSEE: BROWDY
STREET: 419 Seveni
CITY: Washington
STATE: D.C.
                                                                                            D.C.
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US-08-930-996A-2
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	SQUENCE CF LENGTH: TYPE: an TOPOLOGY: 580-327-3	LRDLQVLEYVDIRRISSRAIKELGQLSKLRKLAVITKGS 762	763 TKEKCKILYAAIEKLSSLQSLYMNAALLSDIETLECLDSISSPPPLLRTLGLNGSL-EEM 821 Db 959 LGKLBELLRSKLDLIIDLK 115 :: : : : : :		RTLVIFNLDQLREIRPEDGSSPQLEKIEISCCRLESGIIGIIHLPRLK 929 1073	837 SSKKPFNSLVKLRFEDMPEWKQWHTLGIGEFPTLEKLSIKNCP 879 Qy 181 ANDGP-AKVICVVGMGGLG		DD 1168 NDVLEPSDRNEKEDGE US-08-680-327-3 QY 300 FPKNNKKGSRIVITTRNVD		, Oldroyd, Giles Edward, ommens, Caius	TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PLANT TITLE OF INVENTION: PATHOGEN RESISTANCE TITLE OF INVENTION: 15 Qy 418 VTLGYNHLIPSHLKPCFLYL	1331	Trade Center Qy	Suite 1600 Db 1391	STATE: Oregon STATE: Oregon Gy 536 HIAFHGSMSCKTGLD-W COUNTRY: United States of America	oc A	Db 1498	TWARKE WOIGPETISC 5.1 ON 635 SSTYIAALPSEISKLOCLH ATAPATON WINNERS HE COLOR 500 201	AFFILCALION NOMBER: 05/05/050,52/ FILING DATE: 05/05/050,52/ CLASSIFICATION: 800 LECTION OF THE PARTY OF THE	APPLICATION DATA OY 695 AKQIAEFHMATKSFWSESF ATAPATON MIMMED A 04/210 012	DD 1599ETRSTPRLFYKD- STIP STIP STIP STIP STIP STIP STIP STIP	APPLICATION 000 00 755 LAVITKGS APPLICATION UNBER: 08/227,360 FILING DATE: Abril 13, 1994	CLASSIFICATION: 800 1625 LSCIFSGTFGYSRKLKGRC ATTORNEY/AGENT INFORMATION:	B: Dow, Alan. E. Cy 809 LRTLGLNGSLEEMPNWIED ISTRATION NUMBER: 35,123	CKET NUMBER: 5151-45038 Db 1670 ION INFORMATION:	TELEPHONE: (503) 226-7391 68 GEKIVPKTGAPPNIATIVI DY 868 GEKIVPKTGAPPNIATIVI DY 1013) 228-9446
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--PKV-----HIESQTLFRQLV-KLRERHRIAIRIHNLKSRVE 120
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LMYKVLMISBVLENIKLVNKVVGETCERRNIEVTVHEV---- 1072
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SEIADELRRF------LLTKRFLILLDDVWDYKVWDNLCMCF 1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:|| : | :|| : :| : :|| :|
NDVAEYVKCESDPHHLRLFRDDESWTLLQKGV---FQGESCPP 1272
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|PSRSNVRSL-----LFNAIDPDNLLWPRDISFIFESFK 1497
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|------AEKVLRKMPKLRK 1624
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                                                                                             /EKDIWYIKDELKTMQAFL-RAABVMKKKDELLKVWAEQIRDL
; Score 575; DB 2; Length 1824;
; Pred. No. 7.1e-40;
188; Mismatches 378; Indels 230;
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us-10-656-394a-4.rai

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1391 DLIGRNVVMAMEKRPNTKVKTCRIHDLLHKFCMEKAKQEDF-LLQINSGEGVFPERLEEY 1449
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                                                                      ---LFNAIDPDNLLWPRDISFIFESFK 1497
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                                                                                                                                                                                                               1554 GGEMI---PCSLLKAVV---KLKHIHVNDRVSFGLHENMDVLTGNSQLPNL-----
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                                                                                                                                                                                                                                                                                                                                         755 LAVITKGS-----TKEKCKILYAAIEKLSSLQSLYMNAALLSDIETLECLDSISSPPPL
                                                                                                             578 MLRVLDLEDVTFLITQKDFDRIALLCHLKYLSIGYSSSIYSLPRSIGKLQGLQTL---NM
                                                                                                                                                                                        635 SSTYIAALPSEISKLOCLHTLRCIRELEFDNFSLNHPMKCITNTICLPKVFTPLVSRDNR
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APPLICANT: Kaloshian, Isgouhi
APPLICANT: Kaloshian, Isgouhi
APPLICANT: Yadboobi, Jafar
APPLICANT: Yadboobi, Jafar
APPLICANT: Milligan, Stephen
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Pest Resistance in Plants
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                     536 HIAFHGSMSCKTGLD-W----SIIRSLAIFGDRPKSLAHAVCPDQL
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                                                        986 VPDAQGSVTVAVEATDPLPEQEGES 1010
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APPLICATION NUMBER: PCT/US97/18802
FILING DATE: 09-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/947,823
FILING DATE: 09-0CT-1997
CLASSIFICATION: 800
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/W~
SOFTWARE: Patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08947823; Patent No. 6114605; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 EVSSRNTRYNLVEPISSGTEDDMDSYAEDIRNQSARNVDEAELVGFSDSKKRLLEMIDIN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 ANDGP-AKVICVVGMGGLGKTALSRKIFESEEDIRKNFPCNAWITVSQSFHRIELLKDMI 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VTLGYNHLPSHLKPCFLYLSIFPEDFEIQRNRLVGRWIAEGFVRPKVGMTTKDVGESYFN 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYDIEDSLDE-----FKV-----HIESQTLFRQLV-KLRERHRIAIRIHNLKSRVE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 PPKNNKKGSRIVITTRNVDLAEKCATASLVYHLDFLQMNDAISLLLRKTNKNHEDMESNK 359
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                     926 PRLKEISLEYKSKVARLGQLKGEVNTHPNRPVLRMDSDRRDHDLGAEAEGSSIEVQTADP 985
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                                                                                                                                                                                                                                                                                                        Compositions
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                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: PRF Protein and Nucleic Acid Sequences: Comport Intle OF INVENTION: PRF Protein and Nucleic Acid Sequences: TITLE OF INVENTION: and Methods for Plant Pathogen Resistance FILE REFERENCE: 51700

CURRENT APPLICATION WHERE: US/09/228,246

CURRENT FILING DATE: 1999-01-11

EARLIER PEPLICATION NUMBER: 08/680,327

EARLIER PELING DATE: 1996-07-11

EARLIER PELING DATE: 1994-09-22

EARLIER PELING DATE: 1994-04-13

NUMBER OF SEQ ID NOS: 5

SEQ ID NO 2

LENGTH: 1824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tch 10.9%; Score 575; DB 3; Length 1824; al Similarity 23.8%; Pred. No. 7.1e-40; 249; Conservative 188; Mismatches 378; Indels 230;
                                                                                              986 VPDAQGSVTVAVEATDPLPEQEGES 1010
                                                                                                                     Sequence 2, Application US/09228246
Patent No. 6245510
GENERAL INFORMATION:
APPLICANT: Staskawicz, B. S. et al.
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US-09-228-246-2
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US-09-245-928A-19; Sequence 19, Application US/09245928A; Patent No. 6613962; GENERAL INFORMATION:
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1219 KSPQLEDSALKIK 1231
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US-09-245-928A-19
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                                                                                                                                                                                                         Query Match 10.8%; Score 568; DB 3; Length 1255; Best Local Similarity 25.8%; Pred. No. 1.6e-39; Matches 251; Conservative 165; Mismatches 351; Indels 206;
                                                   023070-070210US
                     NAME: Dation, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 0230
TELECOMMULTATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
FILING DATE: 10-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
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----DSGSSVATNRPWDFHFPSNLKIL----
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TITLE OF INVENTION: RESISTANCE AGAINST NEMATODES AND/OR APHIDS
FILE REFERENCE: 960-35
CURRENT APPLICATION NUMBER: US/09/245,928A
CURRENT PILING DATE: 1999-02-08
FRIOR PILING DATE: 1997-08-08
FRIOR FILING DATE: 1997-08-08
FRIOR FILING DATE: 1997-08-09
FRIOR PILING DATE: 1997-08-09
FRIOR PILING DATE: 1997-05-16
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AENCKGLPLVADLIAGVIAGREKKRSVWLEVQSSLSSFI-LNSEVEVM-KVIELSYDHLP 715
                        SHLKPCFLYLSIFPEDFEIQRNRLVGRWIAEGFVRPKVGMTTKDVGESYFNELINRSMIQ 486
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APPLICANT: KEYGENE N.V.
TITLE OF INVENTION: RESISTANCE AGAINST NEWATODES AND/OR APHIDS
FILE REFERENCE: 960-35
CURRENT FILING DATE: 1995-02-08
CURRENT FILING DATE: 1995-02-08
PRIOR APPLICATION NUMBER: PCT/FP97/04340
PRIOR FILING DATE: 1997-08-08
PRIOR FILING DATE: 1997-08-08
PRIOR FILING DATE: 1996-08-09
PRIOR FILING DATE: 1996-08-09
PRIOR FILING DATE: 1996-08-16
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTING DATE: 1997-05-16
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN VONES: 20
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Patent No. 6613962
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Job time : 36.2998 secs
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Aaz58293 Sorghum r Ada70202 Rice gene Aaax4679 Blast dis Aaa11350 cDNA for Ab150546 Mla1 nucl Ab150547 Mla6 nucl Ab150537 Barley Ml Aaz5062 Coding re Ab25052 Coding re Ab25054 Rghlbcd n Aaz50654 Genomic D Aaz50654 Genomic D Aaz50654 Mla1h nucl Ab150550 Rghla nucl Ab150550 Rghla nucl Ab150550 Rghla nucl Ab150551 Mla1 nucl Ab150551 Mla1 nucl Ab150551 Mla1 nucl Ab150551 Mla1 nucl Ab160542 Barley Ml Ad139841 Plant cDN Ad393713 DNA encod Ad32938 Potatc Me Ad237153 DNA seque Ab150554 Mla Ratial n Aa237153 DNA seque Ab150554 Mla seque Ab150554 Mla seque

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New rice Pi2-like disease resistance nucleic acid molecule that confers disease resistance in plants, useful for creating or enhancing disease resistance in plants.
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                             Location/Qualifiers
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18-MAR-2003; 2003US-0455713P.
05-SEP-2003; 2003US-00656394.
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The invention relates to novel broad-spectrum resistance gene Pi2 and the NBS(1-6) genes present in the Pi2 gene cluster region. The rice Pi2-like disease resistance nucleic acid molecules are useful for enhancing disease resistance in plants. The present sequence represents a cDNA encoding a rice NBS2 polypeptide.
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The invention comprises the amino acid and coding sequences of nucleotide binding site (NBS) proteins from the Oryza minuta Pi9 locus (bacterial blight and rice blast resistance genes). The DNA sequences may be used as markers for resistance to infection with Magnaporthe grises in plant breeding programs. The present DNA sequence represents an NBS gene from the Oryza minuta Pi9 locus.
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                                                                                  CTTAGAACACTTGTGATTTTCAATTTGGATCAGCTAAGAGAGATCAGATTTGAGGACGGC
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                                                                                                                    The invention relates to novel broad-spectrum resistance gene P12 and the NBS(1-6) genes present in the P12 gene cluster region. The rice P12-like disease resistance nucleic acid molecules are useful for enhancing disease resistance in plants. The present sequence represents a P12
molecule that confers
or enhancing disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTATATCAAAGATGAGCTAAAAACAATGCAGGCATTCCTTAGAGCTGCTGAAGTTATGA
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                                                                                                                                                                                                                                                                                                                                                              GGTATATCAAAGATGAGCTAAAAACAATGCAGGCATTCCTTAGAGCTGCTGAAGTTATGA
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Pred. No. 0;
0; Mismatches
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                                                                                Example 3; SEQ ID NO 13; 120pp; English.
  New rice Pi2-like disease resistance
disease resistance in plants, useful
resistance in plants.
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                                                                                                                                                                                                                                                                             95.3%;
                                                                                                                                                                                                       region contiguous sequence
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Best Local Similarity 99.9
Matches 2955; Conservative
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	Qy 2096 CIGAATITCACAIGGCCACCAAAAGTITCIGGICTGAATCATICGGIGIGAAAGGIACCCA 2 	Qy 2156 AAGGAATAGGTAAGTTGCGAGACTTACAGGTTCTAGAGTATGTAGATATCAGGGGACCA 2 	Qy 2216 GTAGTAGAGCAATCAAAGAGCTGGGGCAGTTAAGCAAGTTGAGGAAATTAGCTGTGATAA 2 	2276 53550	2336	Qy 2396 TAGAITCTAITTCAICTCCTCCTCCTAGGAGACATTGGAITGAAIGGAAGTCTIG 2	2456 53730	2516 53790	Oy 2576 TITCICITIATCAIAATICTIATCAIGGGGAGAAGCIAGIATICAAAACGGGAGGATICC 2	Oy 2636 CAAAICTIAGAACACTIGIGAITITICAATTIGGAICAGTAAGAGAGTOGAITIGAGG 2 	53970	2756	2816	Qy 2876 GAATGGACGGAAGGGATCACGACCTGGGGGCTGAAGCCGAAGGATCTTCTATAG 2	OY 2936 AAGTGCAAACAGCAGATCCTGTTCCTGATGCCCAAGGATCAGTCACTGTAGCAGTGGAAG 2	Qy 2996 CAACGGATCCCCTTCCCGAGCAGGAGAGAGAGCTCGCAGTCGCAGGTGATCACGTTGA 3	Qy 3056 CGACGAATGGTAGCGAAG 3073
52170 CATTICCTAAGAACAATAAGAAGGGCAGTCGAATAGTAATAACCACTCGGAATGTTGATC 52229 956 TAGCGGAGAAGTGTGCCACAGCCTCACTGGTGTACCACCTTGATTTCTTGCAGATGAACG 1015	1016 ATGCCATTTCATTGCTACTGAGAAAACCAAATAAAATCATGAAGACATGGAATCAAATA 1075 	1076 AAAATATGCAAAAGATGGTTGAACGAATTGTAAATAAATGTGGTCGTCTTCCTTTAGCAA 	36 TACTTACAATAGGAGCTGTGCTTGCAACTAAACAGGTGTCAGAATGGGAGAATTCTATG 	AACAACTTCCTTCAGAACTAGAAATAAACCCAAGCCTGGAAGCTTTGAGGGAATGGTGAAAAAACTTCCTTC	CCCTAGGITACAACCACCTACCATCTGAAACCATGCTTTTTGTATCTAAGTATCT	1316 TTCCTGAGGATTTTGAAATACAAAGGAATCGTCTAGTAGGTAG	TIGITAGACCAAAGGITIGGGAIGACGACTAAGGAIGICGGAGAAGGITACITITAAIGAGC	1436 TAATCAACCGAAGTATGATTCAACGATCAAGAGTGGGCACAGCAGGAAAATTAAGACTT 1495 	1496 GTCGAATCCATGATATCATCGGGATATCACAGTTTCAATCTCGAGACAGGAAAATTTG 1555	1556 TATTATTACCAATGGGAGATGGCTCTGATTTAGTTCAGGAAAACACTGGCCACATAGCAT 1615 	1616 TCCATGGGAGTATGTCCTGCAAAACAGGATTGGATTGGA	1676 TTTTTGGTGACAGACCCAAGAGTCTAGCACATGCAGTTTGTCCAGATCAATTGAGGATGT 1735 	1736 TACGGGTCTTGGATCTTGAAGATGTGACATTCTTAATCACTCAAAAAGATTTCGACGTA 1795 	TTGCATTGTTGTGCCACTTGAAATACTTGAGTATTGGATATTCGTCATCCATC	TTCCCAGATCCATTGGTAAACTACAGGGCTACAGACTTTGAACATGTCAAGCACATACA TTCCCAAATCCATTGGTAAACTACAGGCCTACAGACATGTCAAGCACATACAATGCAATACA	TTGCAGCACTACCAAGTGAGATCAGTAAACTCCAATGTCTGCATACTCTTCGTTGTATAA	GAGAGCTTGAATTTGACAACTTTAGTCTAAATCACCCAATGAAGTGCATAACTAAC

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                                                                                     GCTGAGCTTGTTGGGGTTTTCTGACTCCAAGAAAAGGCTGCTTGAAATGATGATCGATACCAAT
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                                                                                                                                    GAAGTGAGTAGCAGGAACACACGCTACAATTTAGTCGAGCCTATTTCCTCCGGCACAGAG
                                                                                                                                                                      GAAGTGAGTAGCAGGAACACGCTACAGTTTAGTCAAGCCTATTTCCTCTGGCACAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to novel broad-spectrum resistance gene Pi2 and the NBS(1-6) genes present in the Pi2 gene cluster region. The rice Pi2-like disease resistance nucleic acid molecules are useful for enhancing disease resistance in plants. The present sequence represents a cDNA encoding a rice NBS4 polypeptide.
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or enhancing disease
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                                                                                                                                                                                                            Pi2; NBS4; plant protectant; gene therapy; rice; disease resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 12; Length 3099;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New rice Pi2-like disease resistance nucleic acid disease resistance in plants, useful for creating resistance in plants.
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Pred. No. 0;
0; Mismatches
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                                                                                                                                                                        minuta NBS4 polypeptide encoding cDNA.
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GAGGATTTTGAAATCAAAAGGAATCGTCTAGTAGGTAGGATGGAT	1441 ARCCGARGIATIC CARCGAT CARGAGA CARCGARGARA ARCCGARGIA 1500	TTACCAATGGGAGATGGCTCTGATTTAGTTCAGAAAACACTCGCCACATAGCATTCCAT	1621 GGGAGTATGCCCGAAACAGGATTGGATTGGAGCATTATTGGATCATTATGCGATATTTT 1680 1621 GGGAGTATGTCCTGCAAAACTGGATTGGATTATTCGATCATTATCTTTTT 1680 1681 GGTGACAGACCCAAGAGCTCTAGCACTTGCAGATCAATTGAGGATGTTACGG 1740 1681 GGTGACAGACCCAAGAGTCTAGCACATGCAGTTGAGGATGTTACGG 1740 1681 GGTGACAGACCCAAGAGTCTAGCACATGCAGTTGAGGATGTTACGG 1740		1801 TIGITGIGCCACTIGAAATACTIGAATATIGGATATIGGATATICGICATCCATATATICACTICCC 1850 1861 AGATCCATTGGTAAACTACAGGCCCTACAGACTTTGAACATGCAGCACACATACAT	GCACTACCAAGTGAGATCAGTAAACTCCAATGTCTGCATACTCTTCGTTGTATAAGAGAG	CTTGAATTTGACAACTTTAGTCTAAATCACCCAATGAAGTGCATAACTAAC	2041 CIGCCTAAAGTATTCAAACCTTTAGTTAGTCGCGATAATCGTGCTGAAACAAATTGCTGAA 2100 2041 CIGCCTAAAGTATCACACCTTTAGTTGGTGGTGATGATCGTGCAAACAAA	ATAGGTAAGTTGCGAGACTTACAGGTTCTAGAGTATGTAGATATCAGGCGGACCAGTAGT	2221 AGAGCAATCAAAGAGCTGGGGCAGTTAAGCAAGTTGAGGAAATTAGCTGTGATAACAAAA 2280 	2281 GGCTCGACAAAGAAAAATGTAAGATACTTTATGCAGCCATTGAGAAGCTCTCTTCCCTC 2340 2281 GGGTCGACAAAGGAAAAATGTAAGATACTTTATGCAGCCATTGAGAAGCTCTCTTCCCTC 2340	2341 CAATCTCTATATGAATGCTGCGTTATTATCAGATATTGAAACACTTGAGTGCCTAGAT 2400 	2401 TCTATTTCATCTCCTCCTCCTACTGAGGACACTCGGGTTGAATGGAAGTCTTGAAGGG 2460 2401 TCTATTTCATCTCCTCCTCCTACTGAGGACACTCGTGTTGGATGGA

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                                                 CATTICCTAAGAACAATAAGAAGGCAGTCGAATAGTAATAACCACTCGGAATGTIGH
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                                                                                                                                                                                                                                                                                                                                                                                                                        235
                                                                                                                                                   The invention comprises the amino acid and coding sequences of nucleotide binding site (NBS) proteins from the Oryza minuta Pi9 locus (bacterial blight and rice blast resistance genes). The DNA sequences may be used as markers for resistance to infection with Magnaporthe grises in plant breeding programs. The present DNA sequence represents the Oryza minuta
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                                                            eic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2 NBS3, useful for producing plants resistant to Magnaporthe grisea
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                                                                                                                                                                                                                                                                                                                                                                                                                      AAAAGAAAGATGAACTATTAAAGGTTTGGGCAGAGCAAATACGTGACCTGTCGTATGACA
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                                                                                                                                                                                                                                                                BP; 22112 A; 16049 C; 16316 G; 21795 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                              DB 12; Length 76272
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                                                                                                                                                                                                                                                                                             92.4%; Score 2862; Dilarity 98.0%; Pred. No. 0; Conservative 0; Mismatches
                                                                                                                         Disclosure; SEQ ID NO 83; 136pp; English.
                              WPI; 2004-121064/12
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357 TGAAGAAGTGAGTAGCAGGAACACACGCTACAATTTAGTCGAGCCTATTTCCTCCGGCAC 416
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Pred. No. 0;
0; Mismatches
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3056 CGACGAATGATAGCGAAG 3073
                                                                                          BP.
                                                                                          standard; DNA; 3276
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01-FEB-2002; 2002US-0353304P.
                                                                                                                                                                                                                                                                                                                     27-JAN-2003; 2003US-00352179
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97.0%;
               CGACGAACGATAGGTCAG
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P-PSDB; ADI57176.
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Best Local Similarity
Matches 2895; Conserv
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             TATGCCTGCCTAAAGTATTCACACCTTTAGTTAGTCGCGATGATCGTGCAAAAACAAATTG
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The invention comprises the amino acid and coding sequences of nucleotide binding site (NBS) proteins from the Oryza minuta Pi9 locus (bacterial blight and rice blast resistance genes). The DNA sequences may be used as markers for resistance to infection with Magnaporthe grises in plant breeding programs. The present DNA sequence represents an NBS gene from Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2 and NBS3, useful for producing plants resistant to Magnaporthe grisea GGTGAAACTTAGAGGGGCCACCGGATCGCTATCCGTATCCACAACCTCAAATCAAGAGT GTATATCAAAGATGAGCTAAAAACGATGCAAGCATTCCTTAGAGCTGCTGAACTTATGAA AAAGAAAGATGAACTATTAAAGGTTTGGGCAGAGCAAATACGTGACCTGTCGTATGACAT AAAGAAAGATGAACTATTAAAAGGTTTGGGCAGAGCAAATACGTGACCTGTCATATGACAT TGAAGATTCCCTTGATGAATTTAAAGTCCATATTGAAAGCCAAACCCTATTTCGTCAGTT TGAAGATTCCCTTGATGAATTTAAGGTCCATATTGAAAGCCAAACCCTATTTCGTCAGTT GTATATCAAAGATGAGCTAAAAACAATGCAGGCATTCCTTAGAGCTGCTGAAGTTATGAA nucleotide binding site; NBS; Pi9 gene; bacterial blight; rice blast; plant breeding; transgenic plant; plant; gene; ds. Gaps Length 3276; ö Sequence 3276 BP; 1028 A; 631 C; 770 G; 847 T; 0 U; 0 Other; Oryza minuta Pi9 locus nucleotide binding site (NBS) gene 88; Indels DB 12;

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AAGATGGTTGAACGAATTGTAAATGTGGTCGTCTACCATTAGCAATACTTACAATA 1146
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                                                                                                The invention relates to novel broad-spectrum resistance gene Pi2 and the MBS(1-6) genes present in the Pi2 gene cluster region. The rice Pi2-like disease resistance nucleic acid molecules are useful for enhancing disease resistance in plants: The present sequence represents a cDNA encoding a rice NBS6 polypeptide.
                      nucleic acid molecule that confers
for creating or enhancing disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATGGTCCGGCCAAGGTAATCTGTGTTTGTGATGGGTGTGTTTAGGCAAGACAGCTCTT
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                                                                                                                                                                                                       Length 2997;
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                                                                                                                                                                             Sequence 2997 BP; 874 A; 607 C; 723 G; 793 T; 0 U; 0 Other;
                                                                                                                                                                                                     76.1%; Score 2359.8; DB 12; Lengt ilarity 95.4%; Pred. No. 0; Conservative 0; Mismatches 117; Indels
                                                                         Claim 1; SEQ ID NO 11; 120pp; English
                      Pi2-like disease resistance resistance in plants, useful
                                                 resistance in plants.
                                                                                                                                                                                                                Best Local Similarity
Matches 2430; Conserv
P-PSDB; ADM72249
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The invention comprises the amino acid and coding sequences of nucleotide binding site (NBS) proteins from the Oryza minuta Pi9 locus (bacterial blight and rice blast resistance genes). The DNA sequences may be used as markers for resistance to infection with Magnaporthe grisea in plant breeding programs. The present DNA sequence represents an NBS gene from the Oryza minuta Pi9 locus.
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                                                                         Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NE and NBS3, useful for producing plants resistant to Magnaporthe grisea infection.
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The invention comprises the amino acid and coding sequences of nucleotide binding site (NBS) proteins from the Oryza minuta Pi9 locus (bacterial blight and rice blast resistance genes). The DNA sequences may be used as markers for resistance to infection with Magnaporthe grisea in plant breeding programs. The present DNA sequence represents an NBS gene from the Oryza minuta Pi9 locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GCCTCCGCCGCCGCCGACGAGGCCACCCTCCTGCTCGGCGCGTCCAGAAGGAGATCTGGTAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2 and NBS3, useful for producing plants resistant to Magnaporthe grisea
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                                                                                                                                                                                                  Oryza minuta Pi9 locus nucleotide binding site (NBS) gene
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Pred. No. 0;
0; Mismatches 812; Indels
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                                            AAGGATCTTCTATAGAAGTGCAAACAGCAGATCCTGT
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01-FEB-2002; 2002US-0353304P.
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Best Local Similarity 71.9%;
Matches 2098; Conservative C
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	GAGGATGACATGCATACCCIACACCIITATICAAGCICATIICCCCITAIAACCACA GAGGATGACATCCTATGCAGAAGACATTCGCAATCAGCTCGAAATGTGGAT GAGGATGAGAGGGATTCCTACCTAGAAGATGCTCGCATCAGTCAG		601 ACTACCCTIGCAAGGAAGGCAIAIGAAAACAAGGAACACAIGAAGAACTTCTCGTGT 657 658 AATGCTTGGATTACAGTGTCACAATCATTTCACAGGATTGAGCTACTTAAAGAATGATA 717 658 TGTGCTTGGATCACTGTGTCTCAGTCATTTGACGGAAAGAAA	718 AGGCAALTICTGGGTGCTGATTCATTAGACTCTTGAAAGATTTAGTGAGATTG 777 778 GTGGTGCAAGTACATCTTCTGAGTAGTACAGAGAGAGAAGAAGAAGAAGAGAGAG	TTTGTTGTTGCTTGAGCCTATGGACGATGGATGGAATTGGATTGATGCTGCT TTTCCTAAGAAGAAGAGGGAGTGGAATAGGAATGGAAT	958 GCGGGGAGAGTGTGCCACAGCCTCACTGGTACACCTTGATTTCTTGCAGATGAACGAT 1017	AATATCCAAAAGATGGTTGAAGGAATTGTAAATAAATGGGTCGTCTACCATTAGCAATA	1138 CTCACAATAGGAGGCATTCTTGCTACTAAGAAGATAATGGAATGGGAAAATTTTACAGA 1197 1198 CAACTTCCTTCAGAACTAGAAATAAACCCAGGAAGCCTTGAGGAAGAATGTGCTGAAGCTTTGAGAAATGAAGACTTGAAGACTTGAAGCCTAGAAGCTAGAAGCTAGAAGCTAGAAGCTAGAAGCTAGAAGCCTAGAAGCCTAGAAGCCTAGAAGCTAGAAGCCTAGAAGCCTAGAAGCTAGAAGCTAGAAGCTAGAAGCTAGAAGCTAGAAGCTAGAAGCTAGAAGCTAGAAGCTAGAAGCTAGAAGCTAGAAGCTAGAAGCTAGAAGCTAGAAGCTAGAAGCTAGAAGCTAGAAGAAACCTAGAAGCTAGAAGAAACCTAGAAGCTAGAAGCTAGAAGCTAGAAGCTAGAAGCTAGAAGCTAGAAGCTAGAAGAAACCTAGAAGCTAGAAGCTAGAAGAAACCTAGAAGCTAGAAGCTAGAAGCTAGAAGCTAGAAGAACCTAGAAG	

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18-MAR-2003; 2003US-0455713P.
05-SEP-2003; 2003US-00656394.
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                                                                                                                                                                                                                                                                 The invention relates to novel broad-spectrum resistance gene Pi2 and the NBS(1-6) genes present in the Pi2 gene cluster region. The rice Pi2-like disease resistance nucleic acid molecules are useful for enhancing disease resistance in plants. The present sequence represents a CDNA
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or enhancing disease
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New rice Pi2-like disease resistance nucleic acid disease resistance in plants, useful for creating resistance in plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1563; DB 12;
Pred. No. 0;
0; Mismatches 815;
                                                                                                                                                                                  Disclosure; SEQ ID NO 1; 120pp; English.
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Matches 2091;
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                                                                                                                                                                                                                                                                                           New rice Pi2-like disease resistance nucleic acid molecule that confers disease resistance in plants, useful for creating or enhancing disease
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95.0%; Pred. No. 0;
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                                           CDNA-21
                                         minuta Pi2 region fragment
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18-MAR-2003; 2003US-0455713P.
05-SEP-2003; 2003US-00656394.
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                                                                                                                                    The invention comprises the amino acid and coding sequences of nucleotide binding site (NBS) proteins from the Oryza minuta Pi9 locus (bacterial blight and rice blast resistance genes). The DNA sequences may be used as markers for resistance to infection with Magnaporthe grisea in plant breeding programs. The present DNA sequence represents an NBS gene from the Oryza minuta Pi9 locus.
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                                                                                                                                                                                                                                       The invention relates to novel broad-spectrum resistance gene Pi2 and the NBS(1-6) genes present in the Pi2 gene cluster region. The rice Pi2-like disease resistance nucleic acid molecules are useful for enhancing disease resistance in plants. The present sequence represents a cDNA encoding a rice NBS3 polypeptide.
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or enhancing disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention comprises the amino acid and coding sequences of nucleotide binding site (NBS) proteins from the Oryza minuta P19 locus (bacterial blight and rice blast resistance genes). The DNA sequences may be used as markers for resistance to infection with Magnaporthe grises in plant breeding programs. The present Oryza minuta DNA sequence was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2 and NBS3, useful for producing plants resistant to Magnaporthe grisea
                                                  AGCACATACATTGCAGCACTACCAAGTGAGATCAGTAAACTCCAATGTCTGCATACTCTT
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ling; transgenic plant; plant; ds.
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Query Match

Sequence 2265 BP; 638 A; 471 C; 558 G; 598 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention comprises the amino acid and coding sequences of nucleotide binding site (NBS) proteins from the Oryza minuta P19 locus (bacterial blight and rice blast resistance genes). The DNA sequences may be used as markers for resistance to infection with Magnaporthe grisea in plant breeding programs. The present Oryza minuta DNA sequence was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACTICCATCAGAACTIGAAAGCAATCCAATCGAACCAATGAAGAAGGTGGTAACCC 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2 and NBS3, useful for producing plants resistant to Magnaporthe grisea
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Pred. No. 2.6e-230;
0; Mismatches 563; Indels
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                                                                                                         Pi9 locus-related DNA
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                 2351
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01-FEB-2002; 2002US-0353304P.
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                 standard;
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(LIUG/) LIU G.
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ISM Oryza sativa (indica cultivar-group)

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An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
Lipublished (2004)

Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80488576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CL964074 11near GSS 21-SEP-2004 OSIFCC010263 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
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/note="Oryza sativa exon trapped genomic sequences
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Larity 84.1%; Pred. No. 0;
Conservative 0; Mismatches
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Rice genomic sequence.
                                                                         CL577632
CB652975
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AZ20238
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AG208890 Oryza sat
CC183774 OR CBa008
CL83740 OR CBa008
CL817958 SCEZRZ101
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SM Oryza sativa (indica cultivar-group)

Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Mididlantae; Streptophyta; Entrantoideae; Oryzae.

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S (Anatophyta; Mango, J., Zhao, H., Yan, L., Jao, Y., Sun, N., Jao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yan, L., Wangc, J., Chen, C., Liu, X., Sun, D., Zhao, H., Yan, L., Wang, X., Deng, X.W. and Wang, J.

An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis

L Onpublished (2004)

Contact: Chen Chen

Department of Bioinformatic

Beijing Institute of Genomics
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    Sciences, Beijing 101300, China
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/organism="Oryza sativa (indica cultivar-/mol type="genomic DNA"

/db ref="texon:39946"

/clone lib="Oryza sativa Express Library"

/note="Oryza sativa exon trapped genomic
                                                                                                                                                                                                                                                                                                                                        Score 1565; DB 9; Length 2
Pred. No. 0;
0; Mismatches 815; Indels
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Chinese Academy of Sciences, Be
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
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Best Local Similarity 71.8%;
Matches 2093; Conservative (
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1920 AGCACTACCAAGTGAGATCAGTAAACTCCAATGTCTGCATACTTTGTTGTATAAGAGA 1979 1923	2097 TGNATTTCACATGGCCACCAAAGTTTCTGGTCTGAATCATTCGGTGTGAAGGTACCCAA 2156	2277 ABANGGCTCGACAAAGGAAAATGTAAGATGCTTTATGCAGAAGCTCTTTT 2336 2283 AAAAGGCCCCACAATAAGAAGTATTTTGTGCAGCCATTGAGAAGCTCTTTT 2336 2283 AAAAGGCCCCACAATAAGAAGTATTCAGATTTTTGTGCAATTGAAACTCTTTT 2342 2337 CCTCCAATCTCTCTATATGAATGCTGCGTTATTATCAGATATTGAAACACTTGAGTGCCT 2396 2343 TCTGCAATCTCTCTCTGTGATGCTGAGGAATTCTCAGATAATGAACACTTGAGTGGCT 2402 2397 AGATTCTATTCATCTCCTCCCCCTGTGAGGATTCTCAGATACTGAATGGAACTCTTGA 2456 2403 CAATTCTATTCATCTCCTCCCCCTACTGAGGAACTCTGAGTGGATCTTGA 2456 2403 CAATTCGATTGACTGACTGCTCCTCCCTCCATTCTTGAAGATCAATTGAATGGAATCTTTGC 2462 2457 AGAGATGCCTAACTCCTCCCTCCCTCCCTCTCTAGAGATCAACTTATGGAGTAG 2516 2411	MARIACACCARACTAGGARACATGCTGATGCTGGTGATGTGTGTTATCCAGATGTGTGTTATCCAGATGTGTGTG	Qy 2697 CGCCACCTCCCCATTGGAAAAGTTACATTGCAATCGGAGT 2766 Db 2703 GGCACCTCGCCAACGAAGATTACAATTTATGCTTGCAATTCGAATTCGAATTACGAATTACGAATTACGAATTACGAATTACAAGATTTACATTACAAAAGT 2762 Qy 2757 TATTGGTATCATTACCTTCCAAGAGATTTCACTTGAATACAAAAGT 2816 Db 2763 TATTGGTATCAACACTTCCAAGACTTAAGATTACTTCGCTTGAATACGAAAGT 2822 Qy 2817 GGCTACGCTCCAAGACTTAAGATTATTTCGCTTGAATATGATGATAAAGT 2822 Qy 2817 GGCTACGCTCGCAAGACGAAACTCACACACCCCCAATCATACTCCCCGTCCTGC 2876 Pl
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Oryza sativa (indica cultivar-group)

Oryza sativa (indica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.

E 1 (bases 1 to 3024)

May.L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,
An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis

L Unpublished (2004)

Contact: Chen Chen

Department of Bioinformatic
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OsIFCCO09286 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
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Chinese Academy of Sciences, Beijing 101300,
18-10-80481559
Fax: 86-10-80488676
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/db_xref="taxon:39946"
/clone lib="Oryza sativa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: chenchen@genomics.org.cn
Rice genomic sequence.
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                                                                                                                    CAATTCACGATGCTAAGAGTCTTGGATCTAGAGAATGCAGTATTTTCAGTGACACAAAAA
  GCATTCCATGGGAGTATGTCCTGCAAAACAGGATTGGATTGGAGCATTATTCGATCATTA
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Orzavia
Oryza ativa (japonica cultivar-group) DNA, clone:NE9007 0 102 1A,
3' flanking sequence of Tos17 insertion in rice strain NE9007,
genomic survey sequence.
AG210016
AG210016.1 GI:32357206
                                                                                                                                                                2740 ATGGAATGTTGCCAGTTGAGATCAGGGATTGTTGGCATCAAGCACCTCGAACAGCTCAAC 2799
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
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[Oryza sativa (japonica cultivar-group)] (BAA90798.1)."
                                  2680 TCCGAACTAAGAGGGATAAGATTTGAGAAGGACGCCTTGCCCCACATGGAAGAATAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                2854 AAGGCGCACCCCAAGACACCCGCATTGCGGCTGCTTCAAGACCGAAGCAAAATCGACTTG
                                                                                                                              ATCTCTTGCTGCAGGTTGGAATCAGGGATTATTGGTATCATTCACCTTCCAAGGCTCAAG
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                                                                                                                                                                                                                                                                                                                                                                                             2848 AACACACACCCAAATCGCCCCGTGCTGCGAATGGACAGTGACGGAAGGGATCACGACCTG
GATCAGCTAAGAGAGCATCAGATTTGAGGACGGCAGCTCACCCCCAGTTGGAAAGATAGAA
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Miyao, A., Tanaka, K. and Hirochika, H.
Direct Submission
Submitted (16-APR-2002) Akio Miyao, National Institute of
Agrobiological Sciences, Molecular Genetics; 2-1-2, Kannondai,
Tsukuba, Ibaraki 305-8862, Japan (E-mail:miyao@affrc.go.jp,
URL:http://tos.nias.affrc.go.jp/, Tel:81-298-38-7020,
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Target Site Specificity of the Tos17 Retrotransposon Shows a Preference for Insertion within Genes and against Insertion is Retrotransposon-Rich Regions of the Genome
Plant Cell 15 (8), 1771-1780 (2003)
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/mol_type="genomic DNA"
/strain="NE9007"
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/db_xref="taxon:39947"
/clone="NB9007 0.102.1A"
/clone="NB9007 product directly amplified from genomic DNA"
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/note="Similar to Similar
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2668
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us-10-656-394a-3.rst

AUTHORS Miyao, A., Murata, K. and Hisochika, H. TITLE Direct Submitted (16.AR-2002) Akio Miyao, National Institute of Agrobiological Sciences, Molecular Genetics, 2-1-2, Kambondai, Agrobiological Sciences, Molecular Genetics, 2-1-2, Kambondai, Tiskuba, Iberaki 305-8662, Japan (8-mail:miyao@affErc.go.jp, URL:http://toe.nias.affErc.go.jp/, Tel:81-298-38-7020, URL:http://toe.nias.affErc.go.jp/, Tel:81-298-38-7020, Location/Qualifiers 1. c.698 Julian	2655 GATTTCAATTTCAATTCAATCAACAGAATTTGAACACGCACCCCAATT 361 GACTTCAATTTCAATTTCAATCAACAGAATTTGAACACGCACCTCACCCCAATT 2715 GGAAAAGATACAACACAACAGAATTTGAATTTGAACACGCACCTCACCCCAATT 421 GGAAAAGATAGAATTCACTTGCTGCAATTGAATTTGGTATTTTTTCATTTCACTTCACCT 2775 TCCAAGGCTCAAGGAGTTTCACTTGAATACAAAAGTAAAGTAGATTTCACTTCACCT 2775 TCCAAGGCTCAAGGAGTTTCACTTGAATACAAAGTAAAGTGGCTAGCTTGCTCACCT 2775 TCCAAGGCTCAAGGAGTTTCACTTGAATACAAAGTAAAGTGGCTAGCTTGCTCACCT 2775 TCCAAGGCTCAAGGAGTTTCACTTGAATACAAAGTAAAGTGGCTTGCTCAGCT 2835 GAACAGGCTCAACACCCCAAATCACCCCGTGCTGCCAAGGTTACATTCACTCAGCT 2835 GAATCACGACCCCAAATTCTCCCGTGCTGCCAATGACCGAAG 2895 GGATCACGACCCCAAATTCTCCCCTGCTGCCCAATGACCGAAG 2895 GGATCACGACCCCAAACAACACCCCAAACAACAAGGAAGACCCAAACACCCAAACACCCCTCCCT
1	RESULT 5 AG208890 LOCUS LOCUS LOCUS Oryza sativa (japonica cultivar-group) DNA, clone:NE4506 0 401_lA, 3 flanking sequence of Tos17 insertion in rice strain NE4506, GEORGE ACCESSION AG208890. GI:32356080 GSS. GOURCE ORGANISM ENATYORS Sativa (japonica cultivar-group) GCS. GOURCE ORGANISM ENATYOR: Virialiplantaes; Streeptophyta; Embryophyta; Tracheophyta; Bhinartoideae; Oryza eativa (japonica cultivar-group) GCANISM ENATYOR: Aidiplantaes; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Ulliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; AUTHOR MATHORS SHINCLIKA, Y., Onosaco, K. and Hirochika, H. TITLE Target Site Specificity of the Tos17 Retrotransposon Shows a Preference for Insertion within Genes and against Insertion in Reference for Insertion within Genes and against Insertion in Reference for Insertion within Genes and against Insertion in Reference of Tos17 Regions of the Genome JOURNAL PUBMED PUBMED PUBMED PUBMED PUBMED PUBMED PUBMED PUBMED PUBMED REFERENCE Lace Strain NEFER GSS 09-AUG-2003 ACCESSION AG208890 AG20890 AG208890 AG20880 AG20880 AG20880 AG20880 AG20880 AG20880 AG20880 AG20880 AG20880 AG20

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OR_CBa0055J06.r OR_CBa Oryza rufipogon genomic clone OR_CBa0055J06
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae;
Birhartoideae; Oryzae; Oryza.
1 (bases 1 to 703)
Kim,H., Yu,Y., Wissotski,M., Yost,D., Stum,D., Rao,K., Luo,M.,
Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and
361 GAAGTGAGTAGCAGGAACACACGCTACAATTTAGTCGAGCCTATTTCCTCCGGCACAGAG 420
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Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Fax: 520 621 1259
Email: http://genome.arizona.edu
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/mol_type="genomic DNA"
/db_xref="taxon:4529"
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FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0055 row: J column: 06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3', genomic survey sequence. CL832740
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                                                                                                                                                           Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Cade; Paricidiplantae; Streptophyta; Embryophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD cade; Panicoideae; Andropogoneae; Sorghum.

E 1 (Dases 1 to 810)

Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Sun, F., Sullivan, R., Harris, K., Eastman, A. and Pratt, L.H.

An Est database from Sorghum: iron-deficient seedlings
Unpublished (2003)
Other Ests: FE1 17 D11 hol. A002
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bloinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db xref="taxon:4558"
/db xref="taxon:4558"
/clone="FEI 17 D11 A002"
/lab host="MIGB-TI phage-resistant E. coli"
/lab host="liron-deficient seedlings"
/clone lib="Iron-deficient seedlings"
/clone lib="Iron-deficient seedlings"
/note="Vector: pME188-FL3; Site_1: XhoI; Site_2: XhoI; The library was prepared from polyA+ RNA from seedlings grown hydroponically and in the absence of added iron. At 8 days of age, roots and shoots were harvested and stored at -80 c until RNA was isolated. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME185-FL3 vector (5-prime DraIII site is CACTGTGTG)
3-prime DraIII site is CACCATGTG). XhoI excises the cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mmpratt@ugg.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & W University;
sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATCAAAGATGAGCTAAAAACAATGCAGGCATTCCTTAGAGCTGCTGAAGTTATGAAAAAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 GATTCCCTTGATGAATTTAAAGTCCATATTGAAAGCCAAACCCTATTTCGTCAGTTGGTG 300
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FEI_17_D11.g1_A002 Iron-deficient seedlings Sorghum bicolor cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATGGCGGAGACGGTGCTGAGCATGGCGAGGTCGCTGGTGGGCAGTGCCATCAGCAAGGCC
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Pred. No. 1.2e-108;
0; Mismatches 188;
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Seg primer: Sug5 (CTTCTGCTCTAAAAGCTGCG).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Sorghum bicolor"
/mol_type="mRNA"
/cultivar="BTx623"
                                                                                                                     Sorghum bicolor (sorghum)
                                                                    CF071622.1 GI:33108281
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/lab host="DH10B" RZ1"
/clone lib="RZ1"
/clone lib="RZ2"
/clone lib="RZ2"
/clone lib="RZ2"
/clone lib="RZ2"
/clone lib="RZ2"

      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u> AGGTTCTAGAGTATGTAGATATCAGCCGGACCAGTAGTAGAGCAATCAAAGAGCTGGGGC</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2243 AGTTAAGCAAGTTGAGGAAATTAGCTGTGATAACAAAAGGCTCGACAAAGGAAAATGTA
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                                                                                                                                                                                                                                                                                                                                                                                                     Email: parruda@unicamp.br
Clone distribution: clone distribution information ca
through the Brazilian Clone Collection Center (BCCC)
http://www.bcccenter.fcav.unesp.br
Plate: 015 row: C column: 04
Seg primer: T7 Promoter Primer.
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Pred. No. 1.8e-86;
0; Mismatches 210; Indels
                                                                                                                                                                                                                                                                                 Universidade Estadual de Campinas
Caixa Poetal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
                                                                                          Ubases 1 to 709)
Vettore, A.L., da Silva, F.R., Kemper, E.L. and The libraries that made SUCEST
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 709
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db xref="texon:4547"
/clone="SCEZRZ1015C04"
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Best Local Similarity 70.1%;
Matches 499; Conservative (
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5', mRNA sequence.
CA147958 GA147958.1 GI:35048518
/clone="OR_CBa0055J06"
/tissue_type="young leaves"
/dev_stage="2 week old seedlings"
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/clone_lib="OR_CBa"
/note="Vector: pAGIBAC1, Site_1: HindIII; Site_2: HindIII;
drk treated 36 hrs before harvest"
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984 GGTGTACCACCTTGATTTCTTGCAGATGAACGATGCCATTTCATTGCTACTGAGAAAAG 1043
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740 bp DNA linear GSS 16-AUG-2004
OR CBa0093P17.f OR CBa Oryza rufipogon genomic clone OR CBa0093P17
S', genomic survey sequence.
                                                                                                                                              121 GACTAAAGATGAGTTGCTTAAACTGATAGATGTCAATACTAATGACGGTCCAGCTAAAGT 180
                                                                                                                                                                                                                 241 AAACAAGGAACACAT---GAAGAACTTCTCGTGTTGTGCTTGGATCACTGTGTCTCAGTC 297
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Oryza rufipogon
Bukaryota; Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; Liliopsida; Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
                                                            61 AGATGCTCGCAATCGATCAGGTAGCAACACTGACGAGTCAGAACTTGTGGGGCTTTGCCAA
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                                                                                                                                                                                                                                                                           AAGCGAAGAAGACATTAGGAAGAACTTCCCTTGCAATGCTTGGATTACAGTGTCACAATC
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                                                                                                       504 CTCCAAGAAAAGGCTGCTTGAAATGATCGATACCAATGCTAATGATGGTCCGGCCAAGGT
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Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
                         AGACATTCGCAATCAATCAGCTCGAAATGTGGATGAAGCTGAGCT
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/dev stage="2 week old seedlings"
/lab_host="DHIOB TI phage resistant"
/clone lib="OR_CBa"
/note="Vector: PAGIBAC1; Site_1: HindIII; Site_2: HindIII;
drk treated 36 hrs before harvest"
                                                                2663 ATTTGGATCAGCTAAGAGAGATCAGATTTGAGGACGGCAGCTCACCCCAGTTGGAAAAGA 2722
                                                                                                                                                                                                                                    TCAAGGAGATTTCACTTGAATACAAAGTAAGTGGCTAGGCTTGGTCAGCTGAAGGGAG 2842
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OR_CBa0089H17.f OR_CBa Oryza rufipogon genomic clone OR_CBa0089H17
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bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
I (Dasea I to 737)
Kim, H., Yu, Y., Wissotski, M., Yost, D., Stum, D., Rao, K., Luo, M.,
Jetty, R., Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and
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                                                                                      538 TAGAAATCAGGCGCTGCATTTTGAAGTCAGGGATTATTGGCATCAAGCACCTTCCAAGGC
                                                                                                                                                                                                                                                            387 CAATTTAGTCGAGCCTATTTCCTC---CGGCACAGAGGATGACATGGATTCCTATGCAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036,
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
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BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0089 row: H column: 17
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Class: BAC ends.
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/mol_type="genomic DNA"
/db_xref="taxon:4529"
/clone="OR_CBa0089H17"
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668 TIACAGTGTCACAATCATTTCACAGGATTGAGCTACTTAAAGATATGATACGCCAACTTC 727
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                                 TGTAAATAAATGTGGTCGT 1122
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GSS.
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drk treated 36 hrs before harvest"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298 ATTTGACAGGAAAGAAATTCTGAAACAAATGATCAGGCAACTTCTGGGTGCTGATTCATT 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       504 CTCCAAGAAAAGGCTGCTTGAAATGATGATACCAATGCTAATGATGGTCCGGCCAAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              564 AATCTGTGTTGTTGGGATGGGTTTTAGGCAAGACAGCTCTTTCGAGGAAGATCTTTGA
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                                                                                                                                              1. .740
| organism="Oryza rufipogon" |
| mol_type="genomic DNA" |
| db xref="taxon:4529" |
| clone="OR_CBa0093P17" |
| fissue type="young leaves" |
| dev_stage="2 week old seedlings" |
| lab host="DH10B TI phage resistant" |
| clone_llb="OR_CBa"
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
PCR PRimers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0093 row: P column: 17
Seg primer: TAA TAC GAC TCA CTA TAG GG
                                                                                                                                  Location/Qualifiers
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Best Local Similarity 69.8
Matches 516; Conservative
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Ba0025003.r OP Ba Oryza punctata genomic clone OP_Ba0025003 3, genomic survey sequence.
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/mol_type="genomic DNA"
/db xref="taxon:4537"
/clone="OPD Ba0025003"
/tissue type="young leaves"
/lab host="PH10B-T1 phage resistant"
/clone lib="OP_Ba"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: sjackson@purdue.edu
Basecalling by phred version 0.020425.c. This sequence was derived
from the raw sequence read by clipping with lucy version 1.19s.
Bases 119-993 of the raw sequence (length 1389) were retained after
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ë
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1 (Dases 1 to 875)
SanMiguel, P., Westerman, R., Kim, H., Yu, Y., Wissotski, M., Yost, D., Stum, D., Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C., Hatfield, J., Soderlund, C., Wing, R. and Jackson, S.A. (OMAP Project - Purdue University and Jackson, S.A. (Contact: Scott A. Jackson Laboratory)
717
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658 AAACATAAGACTTGAAGACATGGAAAATGATGAGGACTTGGGCAGCATAATTACAAAAAT
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915 W. State St., West Lafayette, IN 47907,
Tel: 7654963621
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BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 161000 Std Brror: 0.00
Plates row: 0 column: 03
Seg primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
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/lab.nost="k" coil DH10B"
//lone_INDB="CUGIR Rice BAC Library"
//note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII; Rice is one of two most popular grains in the
world. Half of the world population especially those
inhabiting highly populated areas of the humid tropics
and subtropics, rely on rice as their primary source of
carbohydrate. Monocotyledonous rice is a diploid plant
(21=24) with a happioid genome equivalent of 431 Mbp
(Arumuganathan and Barle, 1991). The relatively small
genome of rice, three times larger than that of
Arabidopsis, makes it suitable for genomic studies. In
order to facilitate positional cloning, physical mapping
and genome sequencing of rice, we have constructed a BAC
library from Oryza sativa, Nipponbare variety. The
library from Cryza sativa, Nipponbare variety. The
library from Cryza sativa, Nipponbare variety. The
library from Cryza sativa, Nipponbare variety. The
library from the isolation a particular sequence
with a probability of 99.9 %. Two high density filters,
each containing 18,432 clones (doubly spotted), represent
the whole library for colony screening."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                        /organism="Oryza sativa (japonica cultivar-group)"
/mol type="genomic DNA"
/mol type="genomic DNA"
/db tar="taxon:39947"
/clone="nbxb0093A15r"
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Pred. No. 5e-84;
0; Mismatches 176; Indels
                                                                                                                                                                                                                                                                /tissue_type="Leaf"
/lab_host="E. coli DH10B"
  Seq primer: GGAAACAGCTATGACCATG
                  Class: BAC ends
High quality sequence stop: 2
Location/Qualifiers
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Matches 467; Conservative 0
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bupermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 663)
                                                                                                                                                                                                                                                                                                                     TTGATGACATGTGGAACACACATGACTGGGGAATGGATTAAGGAATTTGCTTTGCCTAGTA
                                                                                TTGGTCCCAGTTCTCTGGATCAACTCTTGCATGAATTGCAAGGGAAGGTGGTGGTGCAAG
                                                                                                                                241 radgrecraarrearrearggaargerreaagggerreaagggaa---ggeaargeaag
                                                                                                                                                                                   TACATCATCTTTCTGAGTACCTGATAGAAGAGCTCAAGGAGAAGAGGTACTTTGTTGTTC
                                                                                                                                                                                                                                     TACCTGACGTTGGTACTTACCTGCAAAATCGGCTGAAAGAATTGAGGTACTTTGTTGTTT
                                                                                                                                                                                                                                                                                        TAGATGATCTATGGATTTTACATGATTGGAATTGGATAAATGAAATTGCATTTCCTAAGA
                                                                                                                                                                                                                                                                                                                                                                                              908 ACAATAAGAAGGGCAGTCGAATAGTAATAACCACTCGGAATGTTGATCTAGCGGAGAAGT
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A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
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100 Jordan Hall, Clemson, S
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
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TITLE
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CL197270 603 bp DNA linear GSS 06-JAN-2004
104 424 10943635 114 32333 078 Sorghum methylation-filtered library
(LibID: 104) Sorghum bicolor genomic clone 10943635, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          598 TATTTACCACCTTGAACCGTTACATATAGATGATGCTATACACTTGCTACTAGCAAAGAC 657
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Specimatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD

(lade; Panicoideae; Andropogoneae; Sorghum.

(bases 1 to 603)

Budiman, M.A., Flick, E., Jones, J., Nunberg, A., Citek, R.W.,

Robbins, D., Rohlfing, T., Bradford, K., Fries, J., McMenamy, J.,

Trani, L., Isak, A., Zimmerman, C., Lakey, N. and Bedell, J. A.

GeneThresher methylation filtered genomic sequences from Sorghum
AAACAAGGAACACAT---GAAGAACTTCTCGTGTTGTGCTTGGATCACTGTGTCTCAGTC 297
                                                                                                                                                  743
                                                                                                                                                                     803
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Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 424 row: c column: 19
Seq primer: M13/pUC Forward
Class: shotgun
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/organism="Sorghum bicolor"
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/cultivar="ATx623"
/db_xref="taxon:4558"
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Unpublished (2004)
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/db xref="taxon:4529"
/db xref="taxon:4529"
/clone="0x CBa0013H04"
/tissue type="young leaves"
/dev stage="2 week old seedlings"
/dev lone="publish of the page resistant"
/clone lib="0x CBa"
/note="vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII;
drk treated 36 hrs before harvest"
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                       CAATCTCGAGACAGGAAAATTTTGTATTATTACCAATGGGAGATGGCTCTGATTTAGTTC 1591
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatrophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 709)
Kim,H., Yu,Y., Wissotski,M., Yost,D., Stum,D., Rao,K., Luo,M.,
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                                           110 CGATTTCTAGAGAGAAAATTTTGTATTCTTACCTAGGGGCACTGACTATGAAGCAGTAC
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University of Arizona
Porbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Eaxi: http://genome.arizona.edu
                                                                                                    1592 AGGAAAACACTCGCCACATAGCATTCCATGGGAGTATGTCCTGC 1635
                                                                                                                                FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0013 row: H column: 04
Seg primer: TAA TAC GAC TCA TAG GG
Class: BAC ends.
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Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
                                                                                                                                                                                                                                                                                                                                    CL801486.1 GI:51027447
                                                                                                                                                                                                                                                                                                                                                                                Oryza rufipogon
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Best Local Similarity
Matches 499; Conserv
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GTCCAGATCAATTGAGGATGTTACGGGTCTTGGATCTTGAAGATGTGACATTCTTAATCA 1774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: leaf, Vector: pBCSK(-); Site_1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to the fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into B. coli cells. This is a methylation-filtered library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="10943635"
/clone_lib="Sorghum methylation-filtered library (LibID:
                                    Budiman, M.A., Flick, E., Jones, J., Nunberg, A., Citek, R.W., Robbins, D., Rohlfing, T., Bradford, K., Fries, J., McMenamy, J., Trani, L., Isak, A., Zimmerman, C., Lakey, N. and Bedell, J.A. GeneThresher methylation filtered genomic sequences from Sorghum
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Pred. No. 2.6e-75;
); Mismatches 145; Indels
  Andropogoneae; Sorghum.
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                                                                                                                                                                                                                                                                                                                                                                                             1. .551
/organism="Sorghum bicolor"
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                                                                                                                                                          Contact: Bedell JA
Orion Genomics, LLC
Orion Genomics, LLC
Tel: 314 615 6979
Pax: 314 615 5975
                                                                                                                                                                                                                                                              Email: jbedell@oriongenomics.com
plate: 424 row: c column: 19
Seq primer: T3 Reverse
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High quality sequence stop: 5
Location/Qualifiers
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/cultivar="ATx623"
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Best Local Similarity 73.7%;
Matches 406; Conservative (
Panicoideae;
                     (bases 1 to 551)
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Unpublished (2004)
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                                                       fiote="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA prepared from purified nuclei was randomly_sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into B. coli cells. This is a methylation-filtered library."
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Sorghum bicolor
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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                   /clone_lib="Sorghum methylation-filtered library (LibID: 104)"
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                                                                                                                                                                                                                              DB 9; Length 603;
                                                                                                                                                                                                                            Score 342.8; DB 9; Length
Pred. No. 8.4e-82;
); Mismatches 162; Indels
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73.1%; Pred
0; 7
  clone="10943635"
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Best Local Si
Matches 440
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KEYWORDS
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Search completed: February 13, 2005, 12:24:41 Job time : 6403.15 secs

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Sequence 4, Appli
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APPLICANT: Iwamoto, Masao
APPLICANT: Katayose, Yuichi
APPLICANT: Sasaki, Takuji
APPLICANT: Wang, Zi-Xuan
APPLICANT: Yamanouchi, Utako
APPLICANT: Ishimaru, Lisa
APPLICANT: Ishimaru, Lisa
APPLICANT: Ishimaru, Lisa
CORRESPONDENCES: 13
CORRESPONDENCE ADDRESS:
US-08-947-823-4
US-09-245-928A-15
US-09-32-86A-1
US-08-588-983-15
US-09-806-7088-22
US-09-806-7088-22
US-09-806-7088-22
US-09-806-7088-22
US-09-949-016-16369
US-09-621-976-2813
US-09-734-674-3
US-09-734-674-3
US-09-734-674-3
US-09-336-946B-34
US-09-349-016-13173
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US-09-94-016-13173
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COUNTRY: USA

ZIP: 0110-2804

ZIP: 0110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/330,330

FILING DATE: 11-JUN-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 10-181455
FILING DATE: 12-JUN-1998
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 34.919
REFERENCE/DOCKET NUMBER: 06501/032001
TELECOMMUNICATION INFORMATION:
TELEFAX: 617/542-5070
TELEFAX: 617/542-5070
INFORMATION FOR SEQ ID NO: 2:
LENGTH: 3925 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 2, Application US/09330330
; Patent No. 6274789
; GENERAL INFORMATION:
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STRANDEDNESS: double
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(cgn2_6/ptodata/1/ina/5A_COMB.seq:*
(cgn2_6/ptodata/1/ina/5B_COMB.seq:*
(cgn2_6/ptodata/1/ina/6A_COMB.seq:*
(cgn2_6/ptodata/1/ina/6B_COMB.seq:*
(cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
(cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
                                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Perfect score:
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1802 TGTTGTGCCACTTGAAATACTTGAGTATTGGATATTCGTCATCCATATATTCACTTCCCA 1861
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                                                                                                                                                                    1922 CACTACCAAGTGAGATCAGTAAACTCCAATGTCTGCATACTCTTCGT 1968
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APPLICANT: Katayose, Yuichi
APPLICANT: Sasaki, Takuji
APPLICANT: Wang, Zi-Xuan
APPLICANT: Wamanouchi, Utako
APPLICANT: Ishimaru, Lisa
TITLE OF INVENTION: RICE GENE RESISTANT TO BLAST DISEASE
                                                                                                                                                                                                            2612 crrigccaaaaccarcarcaagcrrcagaagcracagracarrcar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 111.4; DB 3;
Pred. No. 1.8e-22;
0; Mismatches 471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/330,330
FILING DATE: 11-JUN-1999
PRIOR APPLICATION DATE: 15-JUN-1999
PRIOR APPLICATION NUMBER: JP 10-181455
FILING DATE: 12-JUN-1998
ATTORNEY/AGENT INFORMATION:
NAME: FEASEY, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 06501/032001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06501/032001
                                                                                                                                                                                                                                                                                                                 sequence 3, Application US/09330330 ; Patent No. 62747089 ; PATENTEN INFORMATION: APPLICANT: Yano, Masahiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.6%;
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: Genomic DNA
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 46.9
Matches 426; Conservative
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MEDIUM TYPE: Diskette
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                   4.2%; Score 129; DB 3; L. 46.3%; Pred. No. 3.2e-28; iive 0; Mismatches 620;
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Patent No. 6479731
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bryan, Gregory
APPLICANT: B. 1. du Pont de Nemours and Company
TITLE OF INVENTION: A Pi-ta GENE CONFERRING DISEASE RESISTANCE TO PLANTS
FILE REFERENCE: BB-1136
CURRENT APPLICATION NUMBER: US/09/336,946B
CURRENT PILING DATE: 1999-06-21
PRIOR PRIOR APPLICATION NUMBER: 60/095229
WRIGHT OF SEQ ID NOS: 74
AAATICTATGAACAACTTCCTTCAGAACTAGAAATAAACCCAAGCCTGGAAGCTTTGAGG
                                                          AGAATGGTGACCCTAGGTTACAACCACCTACCATCCCATCTGAAACCATGCTTTTTGTAT
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Sequence 68, Application US/09336946B
; Sequence 66, Application US/09336946B
; Patent No. 6479731
; GREERAL INFORMATION:
; APPLICANT: Bryan, Gregory
; APPLICANT: B. I. du Pont de Nemours and Company
; TITLE OF INVENTION: A Pi-ta GENE CONFERRING DISEASE RESISTANCE TO PLANTS
; FILE REFERENCE: BB-1136
; CURRENT RILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 60/095229
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 68
; LENGTH: 5222
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Pred. No. 5.2e-14;
0; Mismatches 338; Indels
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Best Local Similarity 46.8%;
Matches 308; Conservative (
; SEQ ID NO 3
; LENGTH: 5113
; TYPE: DNA
; ORGANISM: Oryza Bativa
US-09-336-946B-3
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ORGANISM: Oryza sativa
     ; ORGANISM: Or
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| Sequence 57, Application US/09993170
| Patent No. 5743969
| GENERAL INFORMATION:
| APPLICANT: Valent, Barbara
| APPLICANT: Bryan, Gregory
| TITLE OF INVENTION: Modification of a Plant Disease Resistance Gene
| TITLE OF INVENTION: Specificity and Method for Engineering Altered
| TITLE OF INVENTION: Specificity and Method for Engineering Altered
| TITLE OF INVENTION: Specificity
| FILE REFERENCE: BB1385 US NA
| CURRENT FILING DATE: 2001-11-26
| PRIOR FILING DATE: 2000-11-14
| NUMBER OF SEQ ID NOS: 60
| SOFTWARE: Microsoft Office 97
| SEQ ID NO 57
| LENGTH: 5222
| TYPE: DNA
                                                                                                                                    908 ACANTAAGAAGGCCAGTCGAATAGTAATAACCACTCGGAATGTTGATCTAGCGGAGAAGT
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                                                                                                  Gaps
                                                                                                    12;
                                                               Length 5222;
                                                                 Query Match 2.7%; Score 83.2; DB 4; Length 52 Best Local Similarity 46.8%; Pred. No. 5.3e-14; Matches 308; Conservative 0; Mismatches 338; Indels
              ORGANISM: Oryza sativa
 ; TYPE: DNA
; ORGANISM: Ory;
US-09-336-946B-68
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Patent No. 6743969

GRERRAL INFORMATION:
APPLICANT: Valent, Barbara
APPLICANT: Bryan, Gregory
ITILE OF INVENTION: Modification of a Plant Disease Resistance Gene
ITILE OF INVENTION: Specificity and Method for Engineering Altered
ITILE OF INVENTION: Specificity and Method for Engineering Altered
ITILE OF INVENTION: Specificity
FILE REFERENCE: BB1385 US NA
ITILE OF INVENTION: Specificity
FILE REFERENCE: BB1385 US NA
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 60/248,335
PRIOR FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 60
SOFTWARE Microsoft Office 97
SEQ ID NO 60
LENGTH: 5696
ILENGTH: 5696
ILENGTH: 5696
ILENGTH: 5696
ITILE DNA
ORGANISM: Artificial Sequence
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                                                                          Gaps
                                                                          12;
Length 5222;
Score 83.2; DB 4; Length 5 Pred. No. 5.3e-14; 0; Mismatches 338; Indels
Query Match 2.7%;
Best Local Similarity 46.8%;
Matches 308; Conservative
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US-09-336-946B-1

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WS-09-336-946B-1
Sequence 1, Application US/09336946B
Sequence 1, Application US/09336946B
Sequence 1, Application US/09336946B
GENERAL INFORMATION:
APPLICANT: Bryan, Gregory
APPLICANT: E. I. du Pont de Nemours and Company
TITLE OF INVENTION: A Pi-ta GENE CONFERRING DISEASE RESISTANCE TO PLANTS
FILE REFERENCE: BB-1136
CURRENT APPLICATION NUMBER: US/09/336,946B
CURRENT FILING DATE: 1999-06-21
PRIOR PILLING DATE: 1999-06-40
NUMBER OF SEQ ID NOS: 74
SEQ ID NOS: 74
LENGTH: 5757
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                                                                                                                                                                   908 ACAATAAGAAGGGCAGTCGAATAGTAATAACCACTCGGAATGTTGATCTAGCGGAGAAGT
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                 ; OTHER INFORMATION: Description of Artificial Sequence:Chimeric US-09-993-170-60
                                                                               Query Match
2.7%; Score 83.2; DB 4; Length 5696;
Best Local Similarity 46.8%; Pred. No. 5.7e-14;
Matches 308; Conservative 0; Mismatches 338; Indels 12
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ORGANISM: Oryza gativa
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| Sequence 56, Application US/09993170
| Patent No. 6743969
| TITLE OF INVENTION: Modification of a Plant Disease Resistance Gene
| TITLE OF INVENTION: Specificity and Method for Engineering Altered
| TITLE OF INVENTION: Specificity and Method for Engineering Altered
| TITLE OF INVENTION: Specificity and Method for Engineering Altered
| TITLE OF INVENTION: Specificity |
| FILE REPERENCE: BB1385 | NA
| CURRENT FILING DATE: 2001-11-26
| PRIOR APPLICATION NUMBER: 60/248,335
| PRIOR APPLICATION NUMBER: 60/248,335
| PRIOR APPLICATION NUMBER: 60/248,335
| PRIOR PRIOR DATE: 2000-11-14
| NUMBER OF SEQ ID NOS: 60
| SOFTWARE: Microsoft Office 97
| SEQ ID NO 56
| IENGTH: 5757
| TYPE: NA
| ORGANISM: Oryza sativa
| US-09-993-170-56
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                                                                                                 Gaps
Score 83.2; DB 4; Length 5757;
Pred. No. 5.7e-14;
0; Mismatches 338; Indels 12;
    2.7%;
Query Match
Best Local Similarity 46.8<sup>3</sup>
Matches 308; Conservative
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Length 2718;

Score 67.4; DB 3; Length 2 Pred. No. 2.4e-09; 0; Mismatches 281; Indels

Query Match 2.2%; Best Local Similarity 47.8%; Matches 268; Conservative

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821 TCAAGGAGAAGAGGTACTTTGTTGTTCTAGATGATCTATGGATTTTACATGATTGGAATT

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1181 GGGAGAAATTCTATGAACAACTTCCTTCAGAACTAGAAATAAACCCAAGCCTGGAAGCTT

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1361 GGATAGCAGAAGGGTTTGTTA 1381 GGATGGCTGAGGGGTTCCTGA 1303

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1163 GTTCACGTGTGCTTGGGTTGAGTTACGATCACTTGACAAGCGATCTAAAAACATGTCTTC 1222

TGAGGAGAATGGTGACCCTAGGTTACAACCACCTACCATCCCATCTGAAACCATGCTTTT

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3731 ATAATAATAGTTGCAGTAGAATACTAATAACAACAGAAATTGAACCTGTAGCTTTGGCAT 3790
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                                            Gaps
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    DB 4; Length 5757;
Score 83.2; DB 4; Length 5
Pred. No. 5.7e-14;
0; Mismatches 338; Indels
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  2.7%;
                     Best Local Similarity 46.8
Matches 308; Conservative
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Query Match 2.2%; Score 67.4; DB 4;
Best Local Similarity 47.8%; Pred. No. 2.4e-09;
Matches 268; Conservative 0; Mismatches 281;
              Sequence 4, Application US/09864680A
Patent No. 6762285
GENERAL INFORMATION:
APPLICANT: Staskawicz, Brian J
APPLICANT: Dahlbeck, Douglas
TITLE OF INVENTION: BB2 RESISTANCE GENE
TITLE REFERENCE: 42250/234021 (5830-4A)
CURRENT APPLICATION NUMBER: US/09/864,680A
CURRENT PILING DATE: 1999-07-23
PRIOR APPLICATION NUMBER: US 60/093,957
PRIOR FILING DATE: 1998-07-23
SPRIOR FILING DATE: 1998-07-23
SPRIOR FILING DATE: 1998-07-23
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Capsicum annuum
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LENGTH: 2718
US-09-864-680A-4
                                                                                                                                                                                                                                               TITLE OF INVENTION: B82 Resistance Gene FILE REFERENCE: 50687
FILE REFERENCE: 50687
CURRENT APPLICATION NUMBER: US/09/360,186
CURRENT FILING DATE: 1999-07-23
EARLIER FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 2718
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TYPE: DNA ORGANISM: Capsicum annuum

; LOCATION: (1)..(2718) US-09-360-186-4

NAME/KEY: CDS

FEATURE:

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2.2%; Score 67.4; DB 4; Length 3099;
Best Local Similarity 47.8%; Pred. No. 2.7e-09;
Matches 268; Conservative 0; Mismatches 281; Indels 12
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Sequence 2, Application US/09864680A
Sequence 2, Application US/09864680A
Sequence 2, Application US/09864680A
Sequence 3, Application US/09864680A
TITLE OF INVENTION: Be2 RESISTANCE GENE
TITLE OF INVENTION: Be2 RESISTANCE GENE
TITLE OF INVENTION: Be2 RESISTANCE GENE
TITLE OF INVENTION: Be2 RESISTANCE
STICK APPLICATION NUMBER: US/09/864,680A
CURRENT APPLICATION NUMBER: US 09/360,186
PRIOR PILING DATE: 1999-07-23
PRIOR APPLICATION NUMBER: US 60/093,957
PRIOR PILING DATE: 1998-07-23
NUMBER: OF SEQ ID NOS: 14
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ORGANISM: Capsicum annuum
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NAME/KEY: CDS
LOCATION: (93)..(2810)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 2
LENGTH: 3099
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  GGATAAATGAAATTGCATTTCCTAAGAACAATAAGAAGGGCAGTCGAATAGTAATAACCA
                                                                                                                                                                                                                                      872 CCCGTAATGAAGAGTAGCTTGTTATGCTGGTGTAGAGAATTTTTCTTTGCGGATGAGCT
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llarity 47.8%; Pred. No. 2.7e-09;
Conservative 0; Mismatches 281; Indels 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: B62 Resistance Gene
FILE REFERENCE: 506877
CURRENT APPLICATION NUMBER: US/09/360,186
CURRENT FILING DATE: 1999-07-23
BARLIER FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 9
SEQ ID NO 2
LENGTH: 3099
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ORGANISM: Capsicum annuum
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; LOCATION: (93)..(2810)
US-09-360-186-2
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Best Local Simil
Matches 268; (
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                                                                                                             2466 ----accarrarcararcaarracaaacrarracaaaacaaarcacaaarcaaca
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  2411 TCATGGATCAAGATGAGAGTTGGAGTCTTTTCAAAAGTGCAGCATTTTCAAGTGA-
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Pred. No. 1.5e-08;
0; Mismatches 281; Indels
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APPLICANT: Bahlbeck, Douglas
APPLICANT: Dahlbeck, Douglas
APPLICANT: Tal, Thomas H
TITLE OF INVENTION: B82 RESISTANCE GENE
FILE REFERENCE: 42250/234021 (5830-4A)
CURRENT APPLICATION NUMBER: US/09/864,680A
CURRENT FILING DATE: 1099-07-23
PRIOR FILING DATE: 1999-07-23
PRIOR FILING DATE: 1998-07-23
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
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Best Local Similarity 47.8%;
Matches 268; Conservative
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                                                                                                                                                                                                                                               ----AGCATTACCATATGAGTTCGAGACTGTTGGAAAGCAAATCGCAGATGAATGTCACG 1134
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GGATAAATGAAATTGCATTTCCTAAGAACAATAAGAAGGGCAGTCGAATAGTAATAACCA 940
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                                                                    CTCGGAATGTTGATCTAGCGGAGAGTGTGCCACAGCCTCACTGGTGTACCACCTTGATT
                                                                                                               964 CCCGTAATGATGAAGTAGCTTGTTATGCTGGTGTAGAGAATTTTTCTTTGCGGATGAGCT
                                                                                                                                                                                                      1024 TCATGGATCAAGATGAGAGTTGGAGTCTTTTCAAAAGTGCAGCATTTTCAAGTGA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Bs2 Resistance Gene FILE REPRENCE: 50687
FILE REPRENCE: 50687
CURRENT APPLICATION NUMBER: US/09/360,186
CURRENT FILING DATE: 1999-07-23
EARLIER APPLICATION NUMBER: 60/093,957
EARLIER FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
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Patent No. 6262343
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US-09-360-186-1
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GTCTACCATTAGCAATACTTACAATAGGAGCTGTGCTTGCAACTAAACAGGTGTCAGAAT 1180
                                                                                                           2522 GGTTACCACTAACTATTGTCGTGGTTGCAGGCTTCTCAAATCTAAAAGGACAATAGAAG 2581
                                                                                                                                                                 1181 GGGAGAAATTCTATGAACAACTTCCTTCAGAACTAGAAATAAACCCAAGCCTGGAAGCTT 1240
                                                                                                                                                                                                                        2582 ATTGGAAAACTGTTGCTAAAGATGTCAAGTCATTCGTCACAAATGATCCTGATGAACGAT 2641
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----AGCATTACCATATGAGTTCGAGACTGTTGGAAAGCAAATCGCAGATGAATGTCACG 2521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Stackawicz, Brian S., Oldroyd, Giles Edward,
ATILE OF INVENTION: PATHOGEN RESISTANCE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Whinston
ADRESSEE: Whinston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Dow, Alan. E.
REGIGTRATION NUMBER: 35,123
REFERENCE FOCKET NUMBER: 35,123
TELEROMUNICATION INFORMATION:
TELEPAK: (503) 226-7391
TELEPAK: (503) 226-7391
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5475 base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/680,327
FILING DATE: July 11, 1996
CLASSIFICATION: B00
PRIOR APPLICATION NUMBER: 08/310,912
PILING DATE: September 22, 1994
CLASSIFICATION NUMBER: 08/227,360
FILING DATE: April 13, 1994
CLASSIFICATION: B00
ATTORNEY APPLICATION: B00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2762 GGATGGCTGAGGGTTCCTGA 2782
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Patent No. 5859321
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Score 57.6; DB 2; Length 54° Pred. No. 4.3e-06; 0; Mismatches 249; Indels
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Best Local Similarity 45.4<sup>1</sup>
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Sequence 97. Appl
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US-10-656-394A-3

Sequence 3, Application US/10656394A

Publication No. US20040210957A1

GENERAL INFORMATION:

APPLICANT: Wang et al.

TITLE OF INVENTION: Cloning and Characterization of the

TITLE OF INVENTION: Droad-spectrum resistance gene Pl2

FILE REFREENCE: 035718/552062

CURRENT APPLICATION NUMBER: US/10/656,394A

CURRENT FILING DATE: 2003-09-05

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FASTERO for Windows Version 4.0
7 US-10-352-179-84

8 US-10-437-963-41016

8 US-10-656-394A-15

8 US-10-656-394A-15

8 US-10-437-963-49433

8 US-10-437-963-49433

8 US-10-437-963-38603

8 US-10-656-394A-5

7 US-10-352-179-96

7 US-10-352-179-96

8 US-10-656-394A-9

8 US-10-437-963-69440

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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
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                                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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	; Publication No. US20040006788A1 ; GENERAL INFORMATION:
1021 MTTCATTGCTACTAGAMANCAMTAMATCATGAGACTGCTACCAMTAMATT 1080 1021 MTTCATTGCTACTGCAMTCATTAMATCATGAGACTGCTACCAMTCAMATT 1080 1021 MTCCAMAGACTGCTACACTTAMATCATGAGACTGCTACCAMTCAMATT 1141 MTCCAMAGACTGCTGCACTTAMATCATGAGACTGCTACCAMTCAMATTCAMATT 1141 MTCCAMAGACTGCTGCACTTAMATCAGACTGCTACACTTCACACT	TTTCACATGGCCACCAAAAGTTTCTGGTCTGAATCATTCGGTGTGAAGGTACCCAAAGGA

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APPLICANT: Wang, Guo-liang APPLICANT: Wang, Guo-liang APPLICANT: Liu, Guifu TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pla FILE REFERENCE: 22727/04108 CURRENT PAPLICATION NUMBER: US/10/352,179 CURRENT PLING DATE: 2003-01-27 PRIOR PAILNG DATE: 2002-01-25 NUMBER OF SEQ ID NOS: 97 SOFTWARE: Patentin version 3.1 SEQ ID NO 88 LENGTH: 3096 TYPE: DNA SORTWARE: CAS NAME/KEY: CDS AMME/KEY:	Query Match 96.1%; Score 2977; DB 17; Length 3096; Best Local Similarity 98.0%; Pred. No. 0; Matches 3013; Conservative 0; Mismatches 60; Indels 0; Gaps 0; Qy 1 ATGGGGAGAGGGTGTGAGGAGAGGTGCTGGTGGCATCAGCAAGGCC 60 Db 1 ATGGCGAGACGGTGCTGAGAGGTGCTGGTGGCATCAGCAAGAGGC 60 Qy 61 GCCTTGCCGCTGCCAATGAGAGAGGAGTGCTCGGTGGGCATCTGGTAT 120 Qy 61 GCCTTGCCGCTGCCAATGAGAGAGAGCTCCTCGGCGTCGAGAAGGACATCTGGTAT 120	Db 61 GCCTCTGCCGCTGCCGATGAGACGAGCCTCCTGCTCGAGAAGGACATCTGGTAT 120	241 GATTCCCTTGATGATTTAAAGTCCATATTGAAGCCAAACCCTATTTCGTCAGTGGTG 241 GATTCCCTTGATGATTTAAAGTCCATATTGAAGCCAAACCCTATTTCGTCAGTTGGTG 301 AAACTTAGAGGCCCACCGGATCGCTATCCGTACCTCAATCAA	CAGAG CAGAG CAGAA VTGAA	Qy 481 GCTGAGCTTGTTGAGTTTTCTGACTCCAAGAAAAGGCTGCTTGAAATGATCGATACCAAT 540 Db 481 GCTGAGCTTGTTGCGTTTTCTGACTCCAAGAAAGGCTGCTTGAAATGATCGATACCAAT 540 Qy 541 GCTAAATGATGGTCGCCAAGGTAATCTGTGTTGTTGTGGATGGGTGGTTTAGGCAAGACA 600 CA 541 GCTAAATGATGGTCGCCAAGGTAATCTGTGTTGTTGTTGTTGTTGTTGTTTTAGGCAAGACA 600	601 GCTCTTTCGAGGAAGATCTTTGAAAGCGAAGAAGAACATTAGGAAGAACTTCCCTTGCAAT 601 GCTCTTTCGAGGAAGATCTTTGAAAGCGAAGAAGATTAGGAAGATTCCCTTGCAAT 601 GCTCTTTCGAGGAAGATCTTTGAAAGCGAAGAAGATTAGGAAGATTCCTTGCATT 61 GCTTGGATTACAGTGTCACAATCATTTCACAGGATTGAGCTACTTAAAGATATGATACGT

Qy 2941 CAAACAGCAGATCCTGTTCCTGATGCCCAAGGATCAGTCACTGTAGCAGGAAGCAACG 3000 Db 2941 CAAACAGCAGATCCTGTTCCTGATGCCGAAGGATCAGTCACTGTAGCAGTGGAAGCAACG 3000 Qy 3001 GATCCCCTTCCCGAGCAGGAGAGAGACGCTCGCAGTCGCAGTGATCACGTTCACGACG 3060 Db 3001 GATCCCCTTCCCGAGCAGGAGAGAGAGCTCGCAGTCGCAGTGATCACGTTCACGACG 3060 Qy 3061 AATGATAGCGAAG 3073 Db 3061 AATGATAGCTAG 3073	PRESULT 4
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Pred. No. 0;
0; Mismatches 118; Indels
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TITLE OF INVENTION: Cloning and Characterization of ITLE OF INVENTION: broad espectrum resistance gene PFILE REFERENCE: 035718/252062
CURRENT APPLICATION NUMBER: US/10/656,394A
CURRENT FILING DATE: 2003-09-05
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastsEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                           ; Sequence 7, Application US/10656394A; Publication No. US20040210957A1; GENERAL INFORMATION:
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Matches 2981; Conservative
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ORGANISM: Oryza minuta
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; NAME/KEY: CDS
; LOCATION: (1)...(3099)
US-10-656-394A-7
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·		RESULT 6 US-10-352-179-83 US-10-352-179-83 Sequence 83. Application US/10352179 Sequence 83. Application No. US20040006788A1 GENERAL INPORMATION: APPLICANT: Wang, Guo-liang APPLICANT: Liu, Guifu FILE REFERENCE: 22727/04108 CURRENT FALING DATE: 2003-01-27 PRIOR RAPLICATION NUMBER: US/10/352,106 PRIOR REPLICATION NUMBER: 60/352,106 NUMBER OF SEQ ID NOS: 97 SOFTWARE: Patentin version 3.1 SEQ ID NO 803.97	TYPE: DNA 1
	1801 TIGHTGTGCACTIGNATACTIGNATITGGTATTCGTCATACTICALTITTCACTTCCC 1860 1861 AGATCCATTGGTAACTACAGGCCTACAGACTTTGAACATGCAGACATACACTTCCC 1860 1861 AGATCCATTGGTAAACTACAGGCCCTACAAACTTGAACATGCCGAGGCAATACATTGCA 1920 1921 GCACTACCAAGAGTCAGAAACTTCCAATGTCTGCATACATTACATAGAGAG 1980 1921 GCACTACCAAGTGAAACTACAGTAAACTCCCAATGCTTGTATAAGAGAG 1980 1921 GCACTACCAAGTGAGATCAGTAAACTCCCAATGTCTGCATACATTAGGACAG 1980 1921 CTAGAATTTGAACTCTAAATCACCCAATGATCTGCATAACTAAC	TITCATTATGACAACTITAGICTAAACCACCCAATGAAGTGCATAACTAACAATTATGAATTATGACTAACAATTATGAATTGCCATAACTAAC	2281 GGCTGACCAAGGAAAANTGTAAGATACTTTATGCAGCCATTGAGAAGCTCTCCCCC 2340 2281 GGCTCGACAAAGGAAAANTGTAAGATACTTTATGCAGCCATTGAGAAGCTCTCCCCC 2340 2341 CAATCTCTCTATATGAATGCTGCGTTATTATCAGATACTTGAGAGCTCTCTTCCCTC 2340 2341 CAATCTCTCTATATGAATGCTGCGGTTATTATCAGATACTTGAGACCTTGAGTGCCTAGAT 2400 2401 TCTATTTCATCTCTCCTCCTCCTCAGAGACACTCGGGTAATGGAACTTTGAGAG 2460 2401 TCTATTTCATCTCCTCCTCCCTACTGAGACACTCGGGTTGAATGGAACTTTGAGGAG 2460 2401 TCTATTTCATCTCCTCCTCCTCCTCAGAGACACTCGGTTGGATGGA
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Matches 2895; Conservative 0; Mismatches 88; Indels 0; Gaps 0; 117 GTATATCAAGGTGAAAAACAATGCAGGCATTCCTTAGAGCTGCTGAAGTTATGAA 176	297 GGTGAAACTTAGAGAGCGCCACCGGATCGCTATCCGTATCCACAACCTCAAATCAAGAGT 356 [AGAGGATGACATGCTATGCAGAAGACATTCGCAATCAATC	654 TGAAGCTGAGCTTGTTGACTCCAAGAAAAGGTTGCTTGAAATGATCCATTGATCCATTGATTCGATACC 713 537 CAATGCTAATGATCGCCCGCCAAGGTAATCTGTGTTGGGATCGGTGGTTTAGGCAA 596 11	GACAGCTCTTGGAGGAAGATCTTTGAAAGCGAAGAAGACATTAGGAAGAACTTCCCTTG CAATGCTTGGATTACAGTGTCACATTCACAGGATTGAGCTACTTAAAGATATGAT CAATGCTTGGATTACAGTGTCACATCATTTCACAGGATTGAGCTACTTAAAGATATGAT CAATGCTTGGATTACAGTGTCACAATCATTTCACAGGATTGAGCTACTCAAAGATATGAT CAATGCTTGGATTACAGTGTCACAAACATTCACAGGATTGAGCTACTCAAAGATATGAT	717 ACGCCAACTTCTTGGTCCCAGTTCTCTGGATCAACTCTTGCATGAATTGCAAGGGAAGGT 776	GGTGGTGCAAGTACATCTTTCTGAGTACCTGATAGAAGAGCTCAAGGAGAAGAGGTA [1014 CITIGITATICA MATERIA MATE	957 AGCGGAQAAGTGTGCCACAGCCTCACTGGTACACCACCTTGATTTCTTGCAGATGAACGA 1016	1017 TGCCATTTCATTGCTACTGAGAAAAACAAATAAAAATCATGAAGACATGGAATCAAATAA 1076 	1077 AAATATGCAAAAGATGGTTGAACQAATTGTAAATAAATGGGTCGTCTACCATTAGCAAT 1136 	1137 ACTTACAATAGGAGCTGTGCTTGCAACTAAACAGGTGTCAGAATGGGAAAATTCTATGA 1196
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0	RESULT 8 US-10-437-963-37316 US-10-437-963-37316 Sequence 37316, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION: APPLICANT: La Rosa, Thomas J. APPLICANT: Cao, Yongwei APPLICANT: Cao, Yongwei APPLICANT: Boukharov, Andrey A. APPLICANT: Boukharov, Andrey A. APPLICANT: Barbazuk, Brad TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B
ACAACTTCCTTCAGAACTAGAAATAAACCCAAGCCTGGAAGCTTTGAGGAGAATGGTGAC	2154 AAAGTITGITGACAACTITAGTCTAAACCACCCAATGAAGTGCATAACTAACACAAT 2213 2213 2214 ATGCCTGCCTAAAGTATCACACCTTTAGTTAGTTAGTCGCGATAATCGCGCAAACAAA
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Pred. No. 0;
0; Mismatches
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 37316
LENGTH: 4596
                                                                                                                       Query Match
Best Local Similarity 96.9%;
Matches 2562; Conservative
                                                                                      CTHER INFORMATION: Clone ID: US-10-437-963-37316
                                                      TYPE: DNA
ORGANISM: Oryza sativa
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Best Local Similarity 95.4%;
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US-10-656-394A-11
; Sequence 11, Application US/10656394A
; Publication No. US20040210957A1
; GENERAL INFORMATION:
    APPLICANT: Wang et al.
    TITLE OF INVENTION: Cloning and Characterization of the
    TITLE OF INVENTION: Droad-spectrum resistance gene Pi2
    FILE REFERENCE: 035718/252062
; CURRENT APPLICATION NUMBER: US/10/656,394A
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastESQ for Windows Version 4.0
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ORGANISM: Oryza minuta
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                               CTAGATTCTATTTCATCTCCTCCTCCCTACTGAGGACACTCGGGTTGAATGGAAGTCTT
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Publication No: US20040006788A1
| GENERAL INPORMATION:
| APPLICANT: Wang, Guo-liang
| APPLICANT: Liu, Guifu
| TITLE OF INVENTYON: Procedures and Materials for FILE FEFRENT 2727/04108
| CURRENT APPLICATION NUMBER: US/10/352,179
| CURRENT FILING DATE: 2003-01-27
| PRIOR FILING DATE: 2002-01-25
| NUMBER OF SEQ ID NOS: 97
| SEQ ID NO 90
| LENGTH: 3220
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US-10-352-179-90
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                                      812; Indels
                    DB 17;
                  Score 1571.8;
Pred. No. 0;
0; Mismatches
                  Query Match 50.7%;
Best Local Similarity 71.9%;
Matches 2098; Conservative
US-10-352-179-84
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                                                                                                           ; OTHER INFORMATION: Clone ID: PAT_MRT4530_44401C.1
US-10-437-963-41016
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                                                                                                                                                      50.6%; Score 1566.6; 71.8%; Pred. No. 0; tive 0; Mismatches
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 41016
LENGTH: 2925
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Matches 2094; Conservative
                                                                      TYPE: DNA
ORGANISM: Oryza sativa
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Publication No. US20040123343A1

GENERAL INFORMATION:

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APPLICANT: Li Ping

APPLICANT: Li Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B
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TGTTGTCCTTGATGACCTATGGACCATAGATGCATGGAATTGGATTCATGATATTGCTTT TCCTAAGAACATAAGAAGGCAGTCGAATAGTAATAACCACTCGGAATGTTGATCTAGC	1080 TATGCAAAAGATGGTTGAACAAAATAAATAAAGTTGAAGAAGAGAGAAAATGAAGAAA 1082 1080 TATGCAAAAGATGGTTGAACAAATAAATAAATGGTGGTCGTCTACCATTAGCAATACT 1139 1083 CTTGGGCATAGTTGAAAAAGGTGTGGTTATTTACCGCTGCTTACT 1142 1140 TACAATAGGAGCTGTTGCAAAAAGGTGTCAGAATGGAAAATTTTATGAACA 1199 1143 CACAATAGGAGCCATTCTTGCTAAGAAGATAATGGAATGGAGAAATTTTACAGAGA 1202	1200 ACTTCCTTCAGAACTAGAAATAAACCCAAGCCTGGAAGCTTTGAGGAGAATGGTGACCCT	1320 TGAGGATTTTGAAATACAAAGGAATCGTCTAGTAGGTAGATGGATAGCAGAAGGGTTTGT 1379	1440 CAACCGAAGTATGATTCAACGATCAAGAGTGGGCACAGCAGGAAAATTAAGACTTGTCG 1499		1680 TGGTGACAGACCCAAGAGTCTAGCACTGTTTGTCCAGATCAATTGAGGATGTTACG 1739	1800 ATTGTTGTGCCACTTGAAATACTTGAGTATTGGATATTCGTCATCCATATATTCACTTCC 1859 1803 GTTGTTGCGCCACATGAAATATTTGAATTTTGCAAGAGCCTCAACTATTTATACACTTCC 1862 1860 CAGATCCATTGGTAAACTACAGGGCCTACAGACTTTGAACATGTCAAGCATACATTGC 1919 1863 AAGGTCCATAGGAAAATTGCAGTGCTTGCAAATTTTGAACATGAGGAAGGCAAATATCTC 1922 1920 AGCACTACCAAGTGAGAACTCCAATGTCTGCATACTTTGTACATAGAAGA 1979 1923 AGCACTACCAAGTGAGATCAGTAAACTCCAATGTCTGCATACTCTTGGTTGTATAAGAGA 1979

2636 2216 GTAAGATACTTTATGCAGCCATTGAGAAGCTCTCTC 2336 CCCTACTGAGGACACTCGGGTTGAATGGAAGTCTTGA 2456 AGCTCACCTCACCTGAAGAAGTTCAACTTATGGAGTAG 2516 2822 TAA---ATCACCCAATGAAGTGCATAACTAACACAAT 2036 CTTTAGTTAGTCGCGATAATCGTGCAAAACAAATTGC 2096 GTTTCTGGTCTGAATCATTCGGTGTGAAGGTACCCAA 2156 CCCGTTGGTCTGATACAAAGGTGTGAGGGTGCCAAG 2162 GCCAGTTAAGCAAGTTGAGGAAATTAGCTGTGATAAC 2276 CTGCGTTATTATCAGATATTGAAACACTTGAGTGCCT 2396 TGCTGATACTTGGGGCACTGCCCAACCTCATGTTCCT 2576 TCAATTTGGATCAGCTAAGAGAGATCAGATTTGAGGA 2696 AGGIAGAAATCTCTTGCTGCAGGTTGGAATCAGGGAT 2756 GCCTCAAGGAGATTTCACTTGAATACAAAAGTAAAGT 2816 GAGAAGTGAACACACCCAAATCGCCCCGTGCTGCG 2876 TACAGGTTCTAGAGTATGTAGATATCAGGCGGACCAG TTGGGGAGAAGCTAGTATTCAAAACGGGAGCATTCCC ACGACCTGGGGGCT 2913

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Pred. No. 0;
0; Mismatches 815;
TITLE OF INVENTION: broad-spectrum resistance FILE REFERENCE: 035718/252062
CURRENT APPLICATION NUMBER: 02/10/656,394A
CURRENT FILING DATE: 2003-09-05
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PASLSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2982
                                                                                                                                                                                               Query Match
Best Local Similarity 71.7%;
Matches 2091; Conservative 0
                                                                                                       TYPE: DNA
ORGANISM: Oryza minuta
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ORGANISM: Oryza minuta
FRATURE:
NAME/KRY: misc_feature
LOCATION: 2014, 2099, 2114, 2154, 2172, 2178, 2199, 2205, 2226, LOCATION: 2268, 2299, 2333, 2339, 2356
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                    Length 2422;
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Pi2
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wang et al.
TITLE OF INVENTION: Cloning and Characterization of the
TITLE OF INVENTION: Cloning and Characterization of the
TITLE OF INVENTION: broad-spectrum resistance gene Pi2;
FILE REPERBINGE: 035718/252062;
CURRENT APPLICATION NUMBER: US/10/656,394A
CURRENT FILIG DATE: 2003-09-05;
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 2422
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Best Local Similarity 95.0%; Pred. No. 0;
Matches 1540; Conservative 0; Mismatches
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             GTGCTTACCGATGGTTTTCTTAACTTCAATAAATTTCAGTGACCGTGTGAAGTTAATTCC
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RESULT 15 US-10-656-394A-15 ; Sequence 15, Application US/10656394A

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සි	21 AGATATCAGGCGGACCAGTAGTAGAGCAATCAAAGAGCTGGGGCAGTTAAGCAAGC
È	2259 GAAAITAGCIGIGATAACAAAAGGCICGACAAAGGAAAAAIGIAAGAIACITIAIGGAGC 2318
qa	781 GAAATTAGGTGTGACAAACGGGTCGACAAAGGAAAAATGTAAGATACTTTATGCAGC 840
È	2319 CATTGAGAGGCCTCTTCCCTCCAATCTCTCTATATGAATGCTGCGTTATTATCAGATAT 2378
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Š i	2439 GTTGAATGGAAGTCTTGAAGAGATGCCTAACTGGATTGAGCAGCTCACTCA
ପ୍ପ	961 GTTGGATGGAATTCTTGAGGAGATGCCTAACTGGATTGAGCAGCTCACTCA
è 5	2499 GTTCAACTTATGGAGTAGTAAATTAAAGGAAGGTAAAAACATGGTGATACTTGGGGGCACT 2558
ò	GCCCAACCTCATGTTCTTTTATCATAATTCTTATCTTGGGAAAAGCTAGTATT 261
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ò	2619 CAAAACGGGAGCATTCCCAAATCTTAGAACACTTGTGATTTTCAATTTTGGATCAGCTAAG 2678
đ	1141 CAAAACAGGAGCATTCCCAAATCTTAGAACTTTGGATTTTGAATTGGATTGGATGAGG 1200
ò	2679 AGAGATCAGATTTGAGGACGGCAGCTCACCCCAGTTGGAAAAGGATAGAAAATCTCTTGCTG 2738
ΩD	1201 AGAGATCAGATTTGAGGACGGCAGCTCACCCCTGTTGGAAAAGATAGAAATAGGCGAGTG 1260
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qq	L CAGGIIGGAAICIGGGAITACIGGIAICAITCACCIICCAAAGCICAAGGAGAITCCAAI 132
È	2799 TGAATACAAAAGTAAAGTGCTAGGTCAGCTGAGGGAGAGAGTGAACACACAC
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à	2859 ARATCGCCCCGGCTGCGAATGGACAGTGACCGAAGGGATCACGACCTGGGGGTGAAGC 2918
q	L AAATCGCCCCGTGCTGCTAATGTACAGTGACCGAAGGTATCACGACCTGGGGGCTGAAGC 1
ò	2919 CGAAGGATCTTCTATAGAAGTGCAAACAGCAGATCCTCTTCCTGATGCCCAAGGATCAGT 2978
qq	CGAAGGATCTTCTATAGAAGTGCAAACAGCAGATCCTGTTCCTGATGCCGAAGGATCAGT 1
ò	2979 CACTGTAGCAGTGGAAGCAACGGATCCCCTTCCCGAGCAGGAGAGAGA
qq	10
š	3039 GCAGGTGATCACGTTGACGACGAATGATAGCGAAGAGATAGGCACAGCTCAAGCTGGCTG
qq	1561 GCAGGTGATCACGTTGACGAACGAAGAGAGAGAGAAGAGCACAGCTCAAGCTGGCTG
ò	3099 A 3099
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Rice prot Barley M1 Rice isop Rx 28, mo Fx 32, mo Potato re Rx 32, mo Protein e Rx 72, mo Rx 72, mo Rx 72, mo Rx 73, mo Protein e Rx 72, mo Protein e Rx 72, mo

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Title: Perfect :

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protein

Run on:

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Minimum DB Maximum DB

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The invention relates to novel broad-spectrum resistance gene Pi2 and the NBS(1-6) genes present in the Pi2 gene cluster region. The rice Pi2-like disease resistance nucleic acid molecules are useful for enhancing disease resistance in plants. The present sequence represents a rice NBS2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pi2; NBS2; plant protectant; gene therapy; rice; disease resistance.
Abbo6875
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100.0%; Score 5255;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1032; Conservative 0; Mismatches
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18-MAR-2003; 2003US-0455713P.
05-SEP-2003; 2003US-00656394.
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              MAETVLSMARSLVGSAISKAASAAANETSLLLGVEKDIWYIKDELKTMQAFLRAAEVMKK
                                                             KDELLKVWAEQIRDLSYDIEDSLDEFKVHIESQTLFRQLVKLRERHRIAIRIHNLKSRVE
                                                                                              EVSSRNTRYNLVEPISSGTEDDMDSYAEDIRNOSARNVDEAELVGFSDSKKRLLEMIDTN
                                                                                                                                                              ANDGPAKVICVVGMGGLGKTALSRKIFESEEDIRKNFPCNAWITVSQSFHRIELKDMIR
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  MAETVLSMARSLVGSAISKAASAANETSLLLGVEKDIWYIKDELKTMQAFLRAAEVMKK
                                               KDELLKVWAEQIRDLSYDIEDSLDEFKVHIESQTLFRQLVKLRERHRIAIRIHNLKSRVE
                                                                                                          EVSSRNTRYNLVEPISGTEDDMDSYAEDIRNQSARNVDEAELVGFSDSKKRLLEMIDTN
                                                                                                                                            ANDGPAKVI CVVGMGGLGKTALSRKI FESEEDIRKNFPCNAWITVSQSFHRIELLKDMIR
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The invention comprises the amino acid and coding sequences of nucleotide binding site (NBS) proteins from the Oryza minuta Pi9 locus (bacterial blight and rice blast resistance genes). The DNA sequences may be used as markers for resistance to infection with Magnaporthe grises in plant breeding programs. The present amino acid sequence represents an NBS protein encoded by a gene from the Oryza minuta Pi9 locus.
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                                                      Oryza minuta Pi9 locus nucleotide binding site (NBS)
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01-FEB-2002; 2002US-0353304P.
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(first entry)
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                                                                                                                                  Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NE and NBS3, useful for producing plants resistant to Magnaporthe grisea
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   25-JAN-2002; 2002US-0352106P.
01-FEB-2002; 2002US-0353304P.
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                                    MOKMVERIVNKCGRLPLAILTIGAVLATKQVSEWEKFYEQLPSELBINPSLEALRRMVTL
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nucleic acid molecules are useful for enhancing in plants. The present sequence represents a rice NBS4
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Local Similarity 94.1%; Pred. No. 0;
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                     LCHLKYLSIGYSSSIYSLPRSIGKLQGLQTLNMSSTYIAALPSEISKLQCLHTLRCIREL
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              The invention relates to novel broad-spectrum resistance gene Pi2 and the NBS(1-6) genes present in the Pi2 gene cluster region. The rice Pi2-like disease resistance nucleic acid molecules are useful for enhancing disease resistance in plants. The present sequence represents a rice NBS6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNANDGPAKVICVVGMGGLGKTALSRKIFESEEDIRKNFPCNAWITVSQSFHRIELLKDM 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KDELLKVWAEQIRDLSYDIEDSLDEFKVHIESQTLFRQLVKLRERHRIAIRIHNLKSRVE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---GRSNGGPVVGWVASGNQSCLAIDSYAEDIRNQSARNVDEAELVGFSDSKKRLLEMID 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New rice Pi2-like disease resistance nucleic acid molecule that confers disease resistance in plants, useful for creating or enhancing disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAETVLSMARSLVGSAISKAASAAANETSLLLGVEKDIWYIKDELKTMQAFLRAAEVMKK
                                                                                                                                                                                                                                                                                                                                                       Pi2; NBS6; plant protectant; gene therapy; rice; disease resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.8%; Score 4140; DB 8; Length 9 82.5%; Pred. No. 0; ive 23; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 12; 120pp; English.
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18-MAR-2003; 2003US-0455713P.
05-SEP-2003; 2003US-00656394.
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                                                                                                                                                                                                           ADM72249 standard; protein;
                                                                                                             1021 NDSEEIGTAQAG 1032
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                                                                                                                                                                                                                                                                                                                                                                                            Oryza minuta.
                                                                                                                                                                                                                                                                                    03-JUN-2004
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The invention comprises the amino acid and coding sequences of nucleotide binding site (NBS) proteins from the Oryza minuta Pi9 locus (bacterial blight and rice blast resistance genes). The DNA sequences may be used as markers for resistance to infection with Magnaporthe grises in plant breeding programs. The present amino acid sequence represents an NBS protein encoded by a gene from the Oryza minuta Pi9 locus.
                                    SGSGYFSIIDNPKECLMITMCLPMVFLTSINPSDRVKLIPEICMSCSTRMSDTKGVRVPR
                                                                                                                                                                                   LLRHMKYLNFARASTIYTLPRSIGKLQCLQILNMREANISALTTEVTKLQNLRSLRCSRR
                                                                                 KLKEGKNMLILGALPNLMFLSLYHNSYLGEKLVFKTGAFPNLRTLVIFNLDQLREIRFED
                                                                                                                                                                                                                  GSSPQLEKIEISCCRLESGIIGIIHLPRLKEISLEYKSKVARLGQLKGEVNTHPNRPVLR
                                                                      GIGKLRDLQVLEYVDIRRISSRAIKELGQLSKLRKLAVITKGSTKEKCKILYAAIEKLSS
                                                                                                                      LQSLYMNAALLSDIETLECLDSISSPPPLLRTLGLNGSLEEMPNWIEQLTHLKKFNLWSS
                       LEFDNFS-LMHPMKCITNTICLPKVFTPLVSRDNRAKQIAEFHMATKSFWSESFGVKVPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleotide binding site; NBS; Pi9 gene; bacterial blight; rice blast;
plant breeding; transgenic plant; plant.
                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza minuta Pi9 locus nucleotide binding site (NBS) protein #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coding nucleotide binding site (NBS) proteins N for producing plants resistant to Magnaporthe
                                                                                                                                                                                                                                                                                 MDSDRRDHDLGAEA-----EGSSIEVQTA 983
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01-FEB-2002; 2002US-0353304P.
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                                                                                                                                                                                                                               The invention relates to novel broad-spectrum resistance gene P12 and the NBS(1-6) genes present in the P12 gene cluster region. The rice P12-11ke disease resistance nucleic acid molecules are useful for enhancing disease resistance in plants. The present sequence represents a rice NBS1 polypeptide.
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                                                                                                                                                          confers
                                                                                                                                                         New rice Pi2-like disease resistance nucleic acid molecule that confere disease resistance in plants, useful for creating or enhancing disease resistance in plants.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DELLKVWAEQIRDLSYDIEDSLDEFKVHIESQTLFRQLVKLRERHRIAIRIHNLKSRVEE
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                                                                                                                                                                                                                                                                                                                             tch 58.3%; Score 3064; DB 8; Length 9 al Similarity 61.9%; Pred. No. 7.1e-242; 613; Conservative 146; Mismatches 222; 'Indels
                                                                                                                                                                                                          Disclosure; SEQ ID NO 2; 120pp; English
                       2002US-0409216P.
2003US-0455713P.
2003US-00656394.
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                                                                                           RQLLGPSSLDQLLHELQGKVVVQVHHLSEYLIEELKEKRYPVVLDDLWILHDWNWINEIA 299
                                                                                                                                                                                                                                                        NMQKMVERIVNKCGRLPLAILTIGAVLATKQVSEWEKFYEQLPSELEINPSLEALRRAVT 419
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                                                                                                                                                                                                                                              PPKNNKKGSRIVITTRNVDLAEKCATASLVYHLDFLOMNDAISLLLRKTNKNHEDMESNK 359
                                                                                                                                                                                                                                                                                                                                                                    INRSMIQRSRVGTAGKIKTCRIHDIIRDITVSISRQENFVLLPMGDGSDLVQENTRHIAF 539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DGSSPQLEKIEISCCRLESGIIGIIHLPRLKRISLEYKSKVARLGQLKGEVNTHPNRPVL 958
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                                                           9
                                                   MAETVLSMARSLVGSAISKAASAAANETSLLLGVEKDIWYIKDELKTMQAFLRAAEVMKK
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 979;
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Query Match 58.1%; Score 3055.5; DB 8; Length Best Local Similarity 62.8%; Pred. No. 3.5e-241; Matches 610; Conservative 143; Mismatches 216; Indels
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The invention comprises the amino acid and coding sequences of nucleotide binding site (NBS) proteins from the Oryza minuta Pi9 locus (bacterial blight and rice blast resistance genes). The DNA sequences may be used as markers for resistance to infection with Magnaporthe grises in plant breeding programs. The present amino acid sequence represents an NBS protein encoded by a gene from the Oryza minuta Pi9 locus.
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plant breeding; transgenic plant; plant.
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49.4%; Score 2595; DB 8;
Best Local Similarity 55.3%; Pred. No. 2.3e-203;
Matches 539; Conservative 164; Mismatches 242;
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The invention comprises the amino acid and coding sequences of nucleotide binding site (NBS) proteins from the Oryza minuta Pi9 locus (bacterial blight and rice blast resistance genes). The DNA sequences may be used as markers for resistance to infection with Magnaporthe grisea in plant breeding programs. The present amino acid sequence represents an NBS protein encoded by a gene from the Oryza minuta Pi9 locus.
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Matches 530; Conservative 144; Mismatches 261; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to novel broad-spectrum resistance gene Pi2 and the NBS(1-6) genes present in the Pi2 gene cluster region. The rice Pi2-like disease resistance nucleic acid molecules are useful for enhancing disease resistance in plants. The present sequence represents a rice NBS3
                HKGKMDTLYSYPE-----ALPPTISPCECCGEFRYWNTSVYRFYFISSSPTED 803
                                                                                                  854
                                                                                                                                      909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New rice Pi2-like disease resistance nucleic acid molecule that confers disease resistance in plants, useful for creating or enhancing disease resistance in plants.
                                                                                                                              SFWSESFGVKVPKGI ---- GKLRDLQVLEYVDIRRTSSRAIKELGQLSKLRKLAVITKGS
                                           TKEKCKILYAAIEKLSSLOSLYMNAALLSDIETLECLDS------ISSPP---
                                                                               - PLLRTLGLNGSLEEMPNWIEQLTHLKKFNLWSSKLKEGKNMLILGALPNLMFLSLYHNS
                                                                                                804 TQVERKSGDALDAAHAPDEVQ------LMEEQTKRRNHVGTCGVAQPHGPLSSFQCL
                                                                                                                   YLGEKLVFKTGAFPNLRTLVIFNLDQLREIRFEDGSSPQLEKIEISCCRLESGIIGIIHL
                                                                                                                                                      PRLKEISLEYKSKVARLGQLKGEVNTHPNRPVLRMDSDRRDHDLGAEAEGSSIEVQTADP
                                                                                                                                                                                                                                                                                                                                 Pi2; NBS3; plant protectant; gene therapy; rice; disease resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 2134.5; DB 8;
Pred. No. 8.1e-166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; SEQ ID NO 6; 120pp; English.
                                                                                                                                                                                                                                                         ADM72243 standard; protein; 660 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                         2002US-0409216P.
2003US-0455713P.
2003US-00656394.
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                                                                                                                                                                                                                                                                                                                                                                                                         2003WO-US027913
                                                                                                                                                                                                                                                                                                              minuta NBS3 polypeptide
                                                                                                                                                                                                                                                                                              (first entry)
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N-PSDB; ADM72242.
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18-MAR-2003; 2
05-SEP-2003; 2
                                                                                                                                                                                                                                                                                                                                                                                                        08-SEP-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 660
                                                                                                                                                                                                                                                                                                                                                   Oryza minuta
                                                                                                                                                                                                                                                                                              03-JUN-2004
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Best Local Similarity

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                                                                                                                                                                                                                                                                                    299 PRNNKKGSRVIVTTRDVGLAKKCTSELLIYQLKPLEINYAKELLLRKANBAIGDMESDKK 358
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                                                                                    AKDGPTKVVCVVGMGGLGKTTIARKIYESKEDIAKNFSCCAWITVSQSFVRVELLKDLMV
                                                                                                                                                                                                                                    KDELLKVWAEQIRDLSYDIBDSLDEFKVHIBSQTLFRQLVKLRERHRIAIRIHNLKSRVE
                                                                                                                       EVSSRNTRYNLVEPISSGTEDDMDSYAEDIRNQSARNVDEAELVGPSDSKKRLLEMIDTN
                                                                                                                                                                                                                                                                        PKNNKKGSRIVITTRNVDLAEKCATASLVYHLDFLOMNDAISLLLRKTNKNHEDMESNKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAETVLSMARSLVGSA I SKAASAAANETSLLLGVEKD I WY I KDELKTMQAFLRAAEVMKK
                                                                                                                                                                                                                        QLLGPSSLDQLLHELQGKVVVQVHLLSEYLIEBLKEKRYFVVLDDLWILHDWNWINEIAF
                                                                                                                                                                                                                                                                                                                        MOKMVERIVNKCGRLPLAILTIGAVLATKQVSEWEKPYEQLPSELBINPSLEALRRMVTL
                                                                                                                                                                                                                                                                                                                                                                                                                        NRSMIQRSRVGTAGKIKTCRIHDIIRDITVSISRQBNFVLLPMGDGSDLVQENTRHIAFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSMSC-KTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLEDVTFLITQKDFDRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene; bacterial blight; rice blast;
plant.
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VLLCHLKYLRIARYRYRSPYIYSLPQSIARLHGLQTLDLGQTYISTLPTQIT 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         600 ALLCHLKYLSIG----YSSSIYSLPRSIGKLQGLQTLNMSSTYIAALPSEIS 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza minuta Pi9 locus nucleotide binding site (NBS) protein #6
7
 Indels
Mismatches 134;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleotide binding site, NBS, Pi9 plant breeding, transgenic plant;
95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JAN-2002; 2002US-0352106P.
01-FEB-2002; 2002US-0353304P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-JAN-2003; 2003US-00352179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
416; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2004006788-A1
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(LIUG/) LIU G.
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The invention relates to the isolation of novel rice blast fungus (Pyricularia grisea; also known as Magnaporthe grisea) resistance genes (Arom rice strain BL-1. The genes are designated Pi-b (AAA11349) and Pi-b, (AAA11351). The genes can be used for creating rice which has high blast fungus resistance. This sequence represents the protein encoded by the Pi gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVSSRNTRYNLVEPISSGTEDDMDSYAEDIRNQSARNVDEAELVGFSDSKK-RLLEMIDT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NANDGPAKVICVVGMGG-LGKTALSRKIPESEEDIRKNFPCNAWITVSQSFHRIELLKDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VNOLHATOGVEALLEKEKTEQDLAKKFNGCVNDRKCLIVLNDLSTIEEWDQIKKCFOKCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LILINNDSQQVQVISVWGMGGLGKTTLVSGVYQSPRLSDKFDKYVFVTIMRPFILVELLRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEATALSVGKSVLNGALGYAKSAFAEEVALQLGIQKDHTFVADELEMMRSFMMEAHEEQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 KDELLKVWAEQIRDLSYDIEDSLDEFKVHIESQTLFRQLVKLRERHRIAIRIHNLKSRVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KGSRIIVSSTQVEVASLCAGQESQASELKQLSADQTLYAPYDKGSQIIEDSVKPVSISDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AITSTNNHTVAHGEIIDDQSMDADEKKVARKSLTRIRTSVGASEESQLIGREKEISEITH
                                                                                                                                                                                                                                                                                                                                                                                       A blast-resistant gene and related genes, useful for creating a rice grade of high blast resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -------HTTOOTSSTDO-----
                                                 blast fungus; Pyricularia grisea; Magnaporthe grisea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                Pi-b from rice,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22.7%; Score 1191; DB 3;
llarity 27.7%; Pred. No. 6.6e-88;
Conservative 208; Mismatches 363;
                                                                                                                                                                                                                                                                              (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
(NORQ ) NORINSUISANSHO NOGYO SEIBUTSU SHIGEN
                blast fungus-resistance protein
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 26; Page 20-23; 36pp; Japanese.
                                                                                                                                                                                                             99JP-00087305
                                                                                                                                                                                                                                             98JP-00235884
                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAA11349, AAA11350.
                                                                                                                                                                                                                                                                                                                                     2000-379868/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 355; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1251 AA;
                                                                 resistance gene
                                                                                                                                       JP2000125885-A.
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                                                                                                      Oryza sativa.
                                                                                                                                                                                                             29-MAR-1999;
                                                                                                                                                                                                                                               21-AUG-1998;
                                                                                                                                                                          09-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                         ų,
                                                                                                                                                                                                           The invention comprises the amino acid and coding sequences of nucleotide binding site (NBS) proteins from the Oryza minuta Pi9 locus (bacterial blight and rice blast resistance genes). The DNA sequences may be used as markers for resistance to infection with Magnaporthe grisea in plant breeding programs. The present amino acid sequence represents an NBS protein encoded by a gene from the Oryza minuta Pi9 locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KDELLKVWAEQIRDLSYDIEDSLDEFKVHIESQTLFRQLVKLRERHRIAIRIHNLKSRVE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KSILLKVWVQQVRDLSYDIEDCLDEFTVHVGSQTLSRQLMKLKDRHRIAVQIRNLRTRIE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QLIGPSSLDQLLHELQGKVVVQVHHLSEYLIEELKEKRYFVVLDDLWILHDWNWINEIAF 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               481 NRSMIQRSRVGTAGKIKTCRIHDIIRDITVSISRQENFVLLPMGDGSDLVQENTRHIAFH 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----DPSRAGVRGEFKSCRIHDIMRDIAISISREENFILLPEGTDYDVVHGNTRHIAFH 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVSSRNTRYNLVEPISSGTEDDMDSYAEDIRNQSARNVDEAELVGFSDSKKRLLEMIDTN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANDGPAKVICVVGWGGLGKTALSRKIFESEEDIRKNFPCNAWITVSQSFHRIELLKDMIR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PKNNKKGSRIVITTRNVDLAEKCATASLVYHLDFLQMNDAISLLLRKTNKNHEDMESNKN 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRININKGSRVIVTTRDVGLAKECTSELLIYRLKPLEITYAKELLLRKANKKIEDMKSDKK 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MQKMVERIVNKCGRLPLAILTIGAVLATKQVSEWEKFYEQLPSELEINPSLEALRRMVTL 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GYNHLPSHLKPCFLYLSIFPEDFEIQRNRLVGRWIAEGFVRPKVGMTTKDVGESYFNELI 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59
                                                                                                      NBS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NI and NBS3, useful for producing plants resistant to Magnaporthe grisea
                                                                                                                                                                                                                                                                                                                                                                                                                                          MAETVLSMARSLVGSAISKAASAANETSLLLGVEKDIWYIKDELKTMQAFLRAAEVMKK
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         98;
                                                                                                                                                                                                                                                                                                                                                                      Query Match 26.4%; Score 1389; DB 8; Length 451; Best Local Similarity 51.7%; Pred. No. 7.5e-105; Matches 282; Conservative 70; Mismatches 95; Indels 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English
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                                                                                                                                                                          ID NO 95; 136pp;
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                                                   2004-121064/12
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                                                                   N-PSDB; ADIS7177
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417 IMRPFILVELLRSLAEQLHKGSSKKEELLENRVSSKKSLASMEDTELTGQLKRLLEKKSC 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLAHAVCPDQLRMLRVLDLEDVTFLITQXDFDRIALLCHLKYLSIGYSSSIYSLPRSIGK 625
                                                                                    The invention relates to novel broad-spectrum resistance gene Pi2 and the NBS(1-6) genes present in the Pi2 gene cluster region. The rice Pi2-like disease resistance nucleic acid molecules are useful for enhancing disease resistance in plants. The present sequence represents an O. minuta Pi2 gene predicted amino acid sequence
                       confers
                      molecule that confers
or enhancing disease
                                                                                                                                                                                                                                                                                    :| :: |:::||:|| || ||:|:: : | : : : : |::|
VAKQMKELRNKVEDVSQRNVRYHLIKGSAKATINSTEQ--SSVIATAIFGIDDARRAAKQ
                                                                                                                                                                                                                                                                                                                                 177 MHPFSPRDFVQSLVNQLHATQGVEALLEKEKTEQDLAKKFNGCVNDRKCLIVLNDLSTIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IAEGFVRPKVGMTTKDVGESYFNELINRSMI---QRSRVGTAGK-IKTCRIHDIIRDITV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IAIRIHNLKSRVEEVSSRNTRYNLVEPISSGTEDDMDSYAEDIRNQSARNVDEAELVGFS
                                                                                                                                                                                                                                                                                                                    DSKK-RILEMIDTNANDGPAKVICVVGMGG-LGKTALSRKIFESEEDIRKNFPCNAWITV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------LKEKRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280 FVVLDDLWILHDWNWINBIAFPKNNKKGSRIVITTRNVDLAEKCATAS-LVYHLDFLQMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIVLDDFSDTSEWDQIKPTLFPL-LEKTSRIIVTTRKENIANHCSGKNGNVHNLKVLKHN
                                                                                                                                                                                                                             48 MQAFLRAAEVMKKKDELLKVWAEQIRDLSYDIEDSLDEFKVHIESQTLFRQLVKLRERHR
                                                                                                                                                                                                                                                                                                                                                                                                                                   EWDOIKKCFOKCRKGSRIIVSSTQVEVASLCAGQESQASELKQLSADQTLYAFYDKGSQI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DAISLLLRKT--NKNHEDMESNKNMOKMVERIVNKCGRLPLAILTIGAVLAT--KOVSEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKFYEQLPSELEINPSLEALRRMVTLGYNHLPSHLKPCFLYLSIFPEDFEIQRNRLVGRW
                                                                                                                                                                                                       356;
                                                                                                                                                                               20.9%; Score 1100; DB 8; Length 1205; llarity 27.2%; Pred. No. 1.8e-80; Conservative 197; Mismatches 346; Indels 356;
                                                                                                                                                                                                                                                                                                                                                                                                             --- LGPSSLDQLLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
for creating
                      rice Pi2-like disease resistance
ease resistance in plants, useful
                                                                   Disclosure, Fig 5; 120pp; English
                                                                                                                                                                                                                                                                                                                                                                 SQSFHRIELLKDMIRQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOG--KVVVQVHHL
                                               resistance in plants.
WPI; 2004-257576/24.
                                                                                                                                                                                           Local Similarity
nes 336; Conserv
                                                                                                                                                           Sequence 1205 AA;
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                                                                                          SISRQENFVLLPMGDGSDLVQENTRHIA----FHGSMSCKTGL-DWSIIRSLAIFGDRPK
                                                                                                                                      SLAHAVCPDQLRMLRVLDLEDVTFLITQKDFDRIALLCHLKYLSIGYSSSIYSLPRSIGK
                                                                                                                                                  LOGLOTLNMSSTYIAALPSEISKLOCLHTLRCIRELEF---DNFSLNHPMK---CITNTI
                                                                                                                                                                                                        LRQLQMLDIRGTYVKALPKTIIKLQKLQYIHAGRKTDYVWEEKHSLMQRCRKVGCICATC
                                                                                                                                                                                                                                                                          GKLRDLQVLEYVDIRRTSSRAIKELGQLSKLRKLAVITKGSTKEKCKILYAAIEKLSSLQ
                                                                                                                                                                                                                                                                                                                                                                  KE-GKNWLILGALPNLMFLSLYHNSYLGEKLVFK---TG-AFPNLRTLVIFNLDQLREIR
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  EKFYEQLPSELEINPSLEALRRMVTLGYNHLPSHLKPCFLYLSIFPEDFEIQRNRLVGRW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene therapy; rice; disease resistance
                                                                                                                                                                                                                              CLP---KVFTPLVSRDNRAKQIAEFHMATKSFWS-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |:|| :: :||:|:: ETAWEEEVQEARRKGGELKRKIREQLARNPNQPII 1204
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2003US-00656394.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pi2; NBS1; plant protectant;
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110 IRIHNLKSRVEEVSSRNTRYNLVEPISSGTEDDMDSYAEDIRNQSARNVDEAELVGFSDS 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIFGSED--RCPLHLKEVSNGILKKCGGLPLAIITVASLLVTKAITKEEWEKMLKSIGSA 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          | | | | :::|:|||||||||| | : | | : | | EQSKCWMKEVRELSYDIEDSIDSFIFSLGCESNSEPRGFKGFVGRCLNLFADAKTRHWIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RDKLIKLLTEREGTTTQLSVVSIVGFGGLGKTTLANEVYQKLEG---QFDYRAFVSVSQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----PDIKKILRHILCQYS----CRECGNNEIWDEQQLINTTRQFLKDKRYFIVIDDIWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELLKVWAEQIRDLSYDIBDSLDE--FKVHIESQT------LFRQLVKLRERHRIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 KKRLLEMI-DINANDGPAKVICVVGMGGLGKTALSRKIFESBEDIRKNPPCNAWITVSQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FHRIELLKOMIRQLLGPSSLDQLLHELQGKVVVQVHHLSEYLIBELKEKRYFVVLDDLWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LHDWNWINEIAFPKNNKKGSRIVITTRNVDLAEKCAT - - ASLVYHLDFLQMNDAISLLLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KTINKNHEDMESNKNMQKMVERIVNKCGRLPLAILTIGAVLATKQVS--EWEKFYEQLPSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GQDMEEIGECYFNELINRSMIQPVGIQYDGRADACRVHDMILDLIISKSVEENFLTL-CG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGSD--LVQENTRHIA--FHG--SMSCKTGLDWSIIRSLAIFG--DRPKSLAHAVCPDQL
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                                                                                                                                                                                                                                                                                                                                                                                                                         3 ETVLSMARSLVGSAISKAASAAANETSLLLGVEKDIWYIKDELKTMQAFLRAAEVMKKKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEINPSLEALRRMVTLGYNHLPSHLKPCFLYLSIFPEDFEIQRNRLVGRWIAEGFVRPKV
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                                                                                                                                                                                                                                                                                                                                                            Indels 133;
                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                        19.8%; Score 1041.5; DB 3; 30.1%; Pred. No. 8.2e-76; tive 193; Mismatches 365;
                                                                                                                                                                                                                                                                                                                            Best Local Similarity 30.1%; Pro
Matches 297; Conservative 193;
                                                                                                                                                                                                                                     Sequence 953 AA;
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Search completed: February 9, 2005, 08:53:09 Job time : 117.873 secs

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2005, 08:37:57; Search time 28.6479 Seconds (without alignments) 3466.067 Million cell updates/sec US-10-656-394A-4 5255 1 MAETVLSMARSLVGSAISKA.....SQVITLTINDSEEIGTAQAG 1032

Perfect score: Sequence:

283416 segs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries seq length: 0 seq length: 200000000 Minimum DB Maximum DB

PIR 79:*
1: pir1:*
2: pir2:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

resistance protein disease resistance protein protein F12N16.25 probable disease r probable disease r hypothetical protein hypothetical protein hypothetical protein hypothetical proteins proteins and proteins proteins and proteins proteins by the protein nematodes resistan root-knot nematode NBS-LRR type resis bacterial blight-r hypothetical prote F7H2.22 protein -hypothetical prote PRM1 homolog (impo PRM1 homolog (impo hypothetical prote disease resistance probable disease r hypothetical prote disease resistance resistance complex disease resistance resistance complex Description SUMMARIES AS7072 T128977 T48899 T48899 T48899 T48188 T48188 T48188 T78188 T78188 T78188 T78188 T78484 T7848 T78484 T78484 T78484 T78484 T78484 T78484 T7848 T7848 T78484 T78484 T7848 T78484 T78484 T78484 T78484 T78484 T78484 T78484 T7848 图 * Query Match Length D 987 827.5 812 798.5 796.5 794.5 784.5 784.5 782 776 776 Result

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ALIGNMENTS

RESULT 1 A57072 disease resis Cispecies: A7. Cispecies: A3. Cispecies: A7. Cispecies: A7. A7.Itle: Strum A, Reference m A, Scause: De A, Rossauce tym A, Residues: De Cigenetics: A, Genetics: A, Gen	RESULT 1 A57072 disease resistance protein RPM1 - Arabidopsis thaliana Cispecies: Arabidopsis thaliana (mouse-ear cress) Cispecies: Arabidopsis thaliana (mouse-ear cress) Cispecies: Arabidopsis thaliana (mouse-ear cress) Cispecies: Ascaladopsis thaliana (mouse-ear cress) Ascaladopsis Ascaladopsis RPM1 gene enabling dual specificity disease resist Ascaladopsis RPM1 gene enabling dual specificity disease resist Ascaladopsis RPM1 gene enabling dual specificity disease resist by Residues: 1-926 cGRA> Ascaladopsis preliminary; nucleic acid sequence not shown Ascaladopsis 1-926 cGRA> Ascalado
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probable disease resistance protein P23H11.10 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: G96621
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.
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                                                                   DITRKRETF------GIGSFNEPRGENITNVRVRQLRRAPPVDQEELVVGLEDDVKIL 172
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                                                                                                                                               L-EMIDINANDGPAKVICVVGMGGLGKTALSRKIFESEEDIRKNFPCNAMITVSQSFHRI
                                                                                                                                                                                      BLIXDMIRQL--LGPSSLDQLLHELQGKVVVQVHHLSBYLIBELKEKRYFVVLDDLWILH
                                                                                                                                                                                                                                                                                                            231 DILIRIIRSLGIVSAEEMEKI-----KMPEEDEELEVYLYGLLEGKNYMVVVDDVMDPD
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                            --- VDEAEL - VGPSDSKKRL
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                            EVSSRNTRYNLVEPISSGTEDDMDSYAEDIRNQSARN---
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Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprotein repeat
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T12977

hypothetical protein T6H20.240 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Decies: Arabidopsis thaliana (mouse-ear cress)
C;Decies: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T12977
R;Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Submitted to the Protein Sequence Database, July 1999
A;Reference number: 217586
A;Accession: T12977
A;Molecule type: DNA
A;Residues: 1-847 cCHIO>
A;Residues: 1-847 cCHIO>
A;Residues: Le47 cCHIO>
A;Residues: Le47 cCHIO>
A;Residues: Le47 cCHIO>
A;Residues: Le47 cCHIO>
A;Reperimental source: cultivar Columbia; BAC clone T6H20
C;Genetics:
A;Gene: ATSP:T6H20.240
A;Map position: 3
C;Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprotein repea
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EDEAWVLPSNKAFPASLEQCRTQNLEPIARKLVERCQGLPLAIASLGSMMSTKKFESEWK 397
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                                                            KPYEQLPSELEINPSLEALRRMVTLGYNHLPSHLKPCFLYLSIFPEDFEIQRNRLVGRWI
                                                                                         AEGFVR PKVGMTTKDVGESYFNELINRSMIQRSRVGTAGKIKTCRIHDIIRDITVSISRQ
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H.; Tallon, Qy B12 LGLNGSLEEMPNWIEQLTHLKKFNLWSSKLKEGKNMLILCALPNIMFLSLYHNSYLGEKL B71	RESULT 4 745590 hypothetical protein F12A12.50 - Arabidopsis thaliana C,5pecies: Arabidopsis thaliana (mouse-ear cress) C; Accession: T45590 C; Accession: T45590 R; Choisner, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sa submitted to the Protein Sequence Database, December 1999 A,7ccssion: T45590 A,7ccssion: T45413314 A,7ccsion: T45412.50 C; Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprotein repeat	Query Match 15.2%; Score 798.5; DB 2; Length 835; Best Local Similarity 28.0%; Pred. No. 7.2e-38; Matches 264; Conservative 169; Mismatches 360; Indels 149; Gaps 33 Qy	SIGG SAK SESI SESI ATTSC	
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, J. Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A; Reference number: A86141; MUID:21016719; PMID:11130712 A; Retauts: preliminary A; Residues: DAA A; Residues: 1-906 <sto> A; Cross-references: UNIPROT:Q9XIFO; GB:AE005173; NID:G5080812; PIDN:AAD39321 C; Genetics: A; Gane: F23411.10 A; Map position: 1</sto>	15.5% Score 812; DB 2; Length 906;	234 LLKDMIRQLLGPSSLDQLLHELQCKVVVQVHHLSFYLIEELKEKRYFVVLDDLWILH 2:	PEDFEIGRNRLVGEWIAEGEV	

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QY 232 IELLKDMIRQLLGPSSLDOLLHELQCKVV-VQVHHLSEYLIEELKERRYFVVLDDLW 287 Db 230 KHYWQ	453 IYDGSTIEDSGEXYLEELVRRNLVIADDNYLSWQSKYCQMHDWMREVCLSKAKEENF 519VLLPWGDGSDLVQENTRHIAFHGSMSCKTGLDWSIIRSLAI 510 LQIIIDPTCTSTINAQSPSRSRRLSIHSGKAFHILGHKNVRSLIVPRFE 560FGDRPKSLAHAVCPDQLRMLRVLDLEDVTPLITQKDFDRIALLCHLKYLSIGVSSIY 562 EDYWIRSASVFHNLTLLRVLDLSWVKFEGGKLPCS-IGGLIHLRYLSL-YEAKVS 618 SLDRSIGKLQGLQTLAMSSTYIAALPSEISKLQCLHTLRCIRELEFDNFSLNHPMKCITN		Gy 947 GEVNTHPNRPVLRMD 961 	RESULT 6 T51185 resistance protein RPP13 [imported] - Arabidopsis thaliana C;\$pecises. Arabidopsis thaliana (mouse-ear cress) C;Date: 28-Unl-2000 #sequence_revision 28-Unl-2000 #text_change 02-Sep-2000 C;Accession: T51185 R;Bittner-Eddy, P.D.; Crute, I.R.; Holub, E.B.; Beynon, J.L. Plant J. 21, 177-188, 2000 A;Fittle: RPP13 is a simple locus in Arabidopsis thaliana for alleles that specify downy A;Reference number: Z25333 A;Accession: T51185 A;Actuus: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-831 <bit> A;Cross-references: BBL;AR209731; PIDN:AAF42831.1 A;Experimental source: cultivar R1d</bit>
Db 464 IEELIDRSLLEAVR-RERGKVMSCRIHDLLRDVAIKKSKELNFVNVYND 511 Qy 536 HIAPHGSMSCKTGLDWSIIRSLAIFGBRPKSLAHAVCPDQLRMLR 580	759 TKGSTKEKCKILYAAIEKLESLOSISYMWAALLSDIETLECLDSISSEPPLIKTLGINGSL 709	RESULT 5 T48899 Gisease resistance protein rpp8 [similarity] - Arabidopsis thaliana Cisecies: Arabidopsis thaliana (mouse-ear cress) Cisecies: Arabidopsis thaliana (mouse-ear cress) Cisecieston: T48899 Cisecieston: T48899 RimCowell, J.M.; Dhandaydham, M.; Long, T.A.; Aarts, M.G.; Goff, S.; Holub, E.B.; Danglant Cell 10, 1861-1874, 1998 A.Title: Intragenic recombination and diversifying selection contribute to the evolution A; Reference number: Z24999; MUID:99030193; PMID:9811794 A; Accession: T48899 A.Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Mesidues: 1-908 cMCD> A; Molecule type: DNA A; Mesidues: 1-908 cMCD> A; Cross-references: EMBL:AF089711; NID:g3901293; PIDN:AAC78631.1; PID:g3901294 A; Experimental source: Columbia C; Genetics: A; Gene: rpp8 A; Miltrons = 293/1; 342/1	A;Description: susceptible allele of a gene that promotes resistance to Peronospora para Query Match 15.2%; Score 796.5; DB 2; Length 908; Best Local Similarity 25.8%; Pred. No. 1.1e-37; Matches 267; Conservative 199; Mismatches 360; Indels 209; Gaps 37;	Qy 8 MARSLVGSAISKAASAAANETSLLIGVEKDIMYIKDELKTMQAFLRAAEVMKKKDELLKV 67 Db 1 MAEAFVSFGLEKLMDLLSRESERLQGIDGQLDGLKRQLRSLQSLLKDADAKKGGSDRVRN 60 Qy 68 WAEQIRDLSYDIEDSLDEF

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Tablesse resistance protein RPPB (validated) - Arabidopsis thaliana disease resistance protein RPPB (validated) - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress)  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 0.2-Un-2000 #sequence_revision 02-Jun-2000  
##xcossion: T48898  
R;McDowell, J.M.; Dhandaydham, M.; Long, T.A.; Aarts, M.G.; Goff, S.; Holub, E.B.; Dangl Plant Cell 10, 1861-1874, 1998  
A;Title: Intragenic recombination and diversifying selection contribute to the evolution A;Reference number: 22499; MUID:99030193; PMID:9811794  
A;Accession: T48898  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Residues: 1-966  
A;Residues: 1-966  
A;Residues: 1-966  
A;Residues: 1-966  
A;Grose-references: EMBL:AF089710; NID:g3928861; PIDN:AAC83165.1; PID:g3928862  
A;Grose-references: Landsberg erecta  
C;Genetics: A;Gene: RPPB  
A;Introns: 293/1; 342/1  
C;Function: A;Description: promotes resistance to Peronospora parasitica
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C;Genetics:
A;Gene: RPPD13
A;Map position: 3
C;Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprotein
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                                                                                                     163;
                                                                        Length 831;
                                                                                                     Conservative 172; Mismatches 357; Indels
                                                                        DB 2;
                                                                        15.1%; Score 794.5; DB 28.1%; Pred. No. 1.2e-37
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protein F12M16.25 [imported] - Arabidopsis thaliana protein F12M16.25 [imported] - Arabidopsis thaliana (mouse-ear cress) ('jpecies: Arabidopsis thaliana (mouse-ear cress) ('jpecies: Arabidopsis thaliana (mouse-ear cress) ('jpecies: O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 ('jAccession: F95573 R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.M.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hujar, L. Mature 408, 816-820, 2000 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizo, M.; Rooney, T.; Rowley, D.; Sakano, H. A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Titles: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719; PMID:11130712
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FNELINRSMIQRSRVGTAGKIKTCRIHDIIRDITVSISRQENFVLLPMGDGSDLVQENTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        877 AFPNLRTLVIFNLDQLREIRFEDGSSPQLEKIEI 910
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A;Molecule type: DNA
A;Residues: 1-1584 <STO>
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                                                                                    LOGLQTLNMSSTYIAALPSEISKLQCLHTLRCIRELEFDNFSLNHPMKCITNTICLPKVF
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                                                                                                                                                                                                                                                                                                                   -----ELGDLVNLEFLFGFSTOHSSVTD
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RESULT 10 H96617 probable disease resistance protein F9K23.6 [imported] - Arabidopsis thaliana

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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: H96617
C;M.: C;M.: Bcker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Juh, S.Y.; Liu, Z.A.; Liuros, J.S.; Maiti, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Liuros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Rraser, C.M.; Venter, J.C.; Davis, R.W.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: H96617
A;Accession: H969
A;Cross-references: UNIPROT:Q9C646; GB:AE005173; NID:g11034973; PIDN:AAG27128:1; GSPDB:GAGenerics:
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ilarity 25.0%; Pred. No. 5.8e-36;
Conservative 197; Mismatches 394; Indels 164;
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                                WAEQIRDLSYDIEDSLDEFKVHIESQT---LFRQLVKLRERHRIAIRIHNLKSRVEEVSS
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173; Mismatches 357; Indels
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G96617

probable disease resistance protein F9K23.7 [imported] - Arabidopsis thaliana C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001 C.Accession: G96617

RESULT 13

RiTheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.D.; Jonkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: G96617
A;Accession: G96617
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-900 <STO>A;Genetics: GB:AR005173; NID:g11034962; PIDN:AAG27117.1; GSPDB:GN00141 repeat A;Gene: F9K23.7 A;Map position: 1 C;Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprotein 120 355 452 637 :| :: || |:: : || |:: :| | |:: | | |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |: || |:: || |:: || |:: || |:: || |:: || |: || |:: || |: || |:: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: | 298 288 407 394 521 513 573 633 693 67 9 WAEQIRDLSYDIEDSLDEF---KVHIESQTLFRQLVKLR----ERHRIAIRIHNLKSRVE CVERIKEIVYDTENMIETFILKEAARKRSGIIRRITKLTCIKVHRWEFASDIGGISKRIS --VEEDDIQIVSVTGMGGLGKTTLARQVF-NHEDVKHQFDRLAWVCVSQEFTRKNVWQMI EVSSRNTRYNLVEPISSGTEDD--MDSYAEDIRNQSARNVDBAELVGFSDSKKRLLEMID TNANDGPAKVICVVGMGGLGKTALSRKIFESEEDIRKNFPCNAWITVSQSFHRIELLKDM 239 IRQLLGPSSLDQLLHBLQGKVVVQVHHLSBYLIEELKEKRYFVVLDDLWILHDWNWINEI AFPKNN----KKGSRIVITTRNVDLAEKCATASLVYHLDFLQMNDAISLLLRKTNKNHEDM ESNKNMOKMVERIVNKCGRLPLAILTIGAVLATKQV-SEWEKPYEQLPSEL-----EI 108 NPSLEALRRMVTLGYNHLPSHLKPCFLYLSIFPEDFEIQRNRLVGRWIAEGFVRPK--VG 466 MITKDVGESYFNELINRSMIQRSRVGTAGKIKTCRIHDIIRDITVSISRQENPV----LL PMGDGSDLVQENTRHIA-----PHGSMSCKTGLDWSIIRSLAIFGDRPKS---LAHAVCP MARSLVGSAISKAASAANETSLLLGVEKDIWYIKDELKTMQAFLRAAEVMKKKDELLKV ------EGRNLPSGIGKLIHLRYLN MSSTYIAALPSEISKLQCLHTLRCIRELEFDNFSLNHPMKCITNTICLPKVFTPLVSRDN Indels 139; 14.1%; Score 741.5; DB 2; Length 900; 1larity 25.4%; Pred. No. 1.5e-34; Conservative 197; Mismatches 389; Indels 139 -RLELLRVLDLYKAKF-----Similarity 247; 356 **&** 236 Query Match Best Local 68 179 299 335 395 453 522 603 g g g g 셤 유 요 ઠે g g 셤 셤 ઠે ò ò ઠે ઠે જે ò ò δ ₹ 셤 ઠ

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hypotherical protein [imported] - Arabidopsis thaliana
CiSpecies: Arabidopsis thaliana (mouse-ear cress)
CiSpacession: A86243
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: A86141; MUID:21016719; PMID:11130712
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384 SSLRVKDDNIHVSSLFDLSFKDMGHELKLCFLYLSVFPEDYEVDVEKLIQLLVAEGFIQE
                                                                                                           LLPMGDGSDLVQENTRHIAFH---GSMSCKTGLDWSIIRSLAIFGDRPKSLAHA-VCPDQ
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                                                                             KVGMTTKDVGESYFNELINRSMIQ----RSRVGTAGKIKTCRIHDIIRDITVSISRQENFV
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("Species: Arabidopsis thaliana (mouse-ear cress)
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("Species: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
("Accession: T12979
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                                                                                                           KLAV-ITKGSTKEKCKILYAAIEKLSSLQSLYM-----NAALLSDIETLECLDSISSPPP 807
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                                 CLMGMHELRYLRLPF---NTSKEIKLGLCNLVNLETLENFS---TENSSLEDLRGMVSLR
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VG18KCS.

01-JUN-2003 (TrEMBLrel. 24, Created)

01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

01-JUN-2003 (TrEMBLrel. 25, Last annotation update)

01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

NGS-LRR disease resistance protein homologue.

Name-rga S-9202;

Hordeum vulgare (Barley).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;

Triticeae; Hordeum.

NCBI_TaxID=4513;
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A Madden L.H., Collins N.C., Rakwalska M., Backes G., Sandal N.,
A Krussell L., Jensen B.H., Jahoor A., Pryor A.J.,
Langridge P., Schulze-Lefert P., Stougaard J.;
T "Barley disease resistance gene analogs of the NBS-LRR class:
identification and mapping.";
Mol. Genet. Genomics 269:150-161(2003).
R EMBL, AJ570794; CAD450310.1;
R GO; GO:0005514; Prypt binding; IEA.
GO; GO:0005515; Prapt binding; IEA.
GO; GO:0005515; Prapt binding; IEA.
GO; GO:0006515; Prapt binding; IEA.
R GO; GO:0005915; Prapt binding; IEA.
R InterPro; IPR000767; Disease resist.
R InterPro; IPR000318; NB-ARC.
R InterPro; IPR00318; NB-ARC.
R InterPro; IPR00314; NB-ARC.
R PRINTS; PR0034; DISEBASESIST.
C SEQUENCE 1014 AA; 114280 MW; 62C3FESF04657332 CRC64;
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069ms5 triticum ae
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                       GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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1: uniprot_sprot:*
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                                                                   PFam; PF00931; NB-ARC; 1.
PRINTS; PR00364; DISEASERSIST.
SEQUENCE 1007 AA; 114793 MW; P96F2CE09AE808E3 CRC64;
                  pathogen; IEA
                                                                                                                                           / Match 48.2%; Score 2532; DB 2; Local Similarity 52.6%; Pred. No. 2.9e-126; nes 541; Conservative 156; Mismatches 289;
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GO; GO:0006915; P:apoptosis; IEA.
GO; GO:0042829; P:defense response t
InterPro; IPR000767; Disease_resist.
InterPro; IPR002182; NB-ARC.
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 OLLGPSSLDQLLHELQGKVVVQVHHLSEYLIEELKEKRYPVVLDDLMILHDWNWINEIAF
                    NRSMIQRSRVGTAGKIKTCRIHDIIRDITVSISRQENFVLLPMGDGSDLVQE-NTRHIAP
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Q1-OCT-2000 (TERMELRE1. 15, Created)
01-OCT-2000 (TERMELRE1. 15, Last sequence update)
01-OCT-2000 (TERMELRE1. 26, Last annotation update)
Similar to gene for Pib.
Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP001168; BAA90798.1; -.
Gramene; Q9LWW7; -.
GO; GO:0005524; F:ATP binding; IEA.
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719 ERPA-VLSEIGQLQKLQXLNVLFRGVEENWNAFLQSLVXLTGSLRSLSIH--ILDEKEHS 775
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             465 IRRGPLVRRWIAEGFVNQRHGLSMEEVAESYFDBFVARSIVQPVKIDWSGKVRTCRVHDM
                                                                                                   IRDITVSISROENFVLLPMGDGSDLV-QENTRHIAFHGSMSC--KTGLDWSIIRSLAIFG
                                                                                                                                                                                                                                                                            562 DRPKSLAHAVCP---DQLRMLRVLDLEDVTFLITQKDFDRIALLCHLKYLSIGYSSSIYS
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Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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llarity 32.9%; Pred. No. 5.18-59;
Conservative 193; Mismatches 355; Indels 132;
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Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6,
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EMBL; AP005828; BAD46435.1; --
SEQUENCE 954 AA; 108010 MW; 0F8BEBBE635D2750 CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to NBS-LRR type resistance gene.
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Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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.larity 33.7%; Pred. No. 9.3e-62;
Conservative 204; Mismatches 339; Indels 127;
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EMBL; AP005828; BAD46438.1; -.
SEQUENCE 953 AA; 108557 MW; DAFD5081E707261C CRC64;
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Last annotation update)
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25-OCT-2004 (TrEMBLrel. 28, Last annotat
Similar to NBS-LRR type resistance gene.
Name=P0702F05.17;
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DDAGESSQ 1002
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Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome
"One:OJ1634 B10.";
Submitted (JŪL-2001) to the EMBL/GenBank/DDBJ database
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                                                                                                                                                                EMBL; APO0340; BAC15497.1; -. Gramene; OBHSA7; -. Go:0005524; F:ATP binding; IEA. GO: GO:0042829; P:ATP binding; IEA. GO: GO:0042829; P:defense response to InterPro; IPR000767; Disease_resist. InterPro; IPR001611; IRA. InterPro; IPR001611; IRA.
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InterPro; IPR008940; Prenyl_trans
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TIGRFAMB; TIGR00756; PPR; 4.
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Pfam; PF00931; NB-ARC; 1.
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CNAWITVSQSFHRIELLKDMIRQL-----LGPSSLDQLLHELQGKVVVQVHH 265
                                                                                                                                                                                                                                                                                                                   429 LKPCFLYLSIFPEDFELORNRIVGRWIAEGFVRPKVGMTTKDVGESYFNELINRSMIQRS 488
                   :||:||:|::|||||||:::||
691 ERRQLVGIEPRQGNLVHWL-LEAHVQQLRVVSIFGFGGLGKITLAMTIYQSLSGRNGPFQ
                                                                                                                                                                                                                                                                                                                                                                                                61 KDELLKVWAEQIRDLSYDIEDSLDEFKVHIESQT-----LFRQ----LVKLRERHR
                                                                       IAIRIHNLKSRVEEVSSRNTRYNLVEPISSGTEDDMDSYAEDIRNQSARNVD-----
                                                                                                                                                                                                                                             LSEYLIEELKEKRYFVVLDDLWILHDWNWINEIAFPKNNKKGSRIVITTRNVDLAEKCAT
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                                                                                                                                                 - EAELVGFSDSKKRLLEMIDTNANDGPAKVICVVGMGGLGKTALSRKIFESEEDIRKNFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         546 KTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLEDVTFLITQKDFDRIALLCHL
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative disease resistance protein RPH8A.
Name=001634 B10.108;
Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantes, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Shrhartoideee; Oryzeae; Oryza.
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PRT; 1494 AA

RESULT 5
08H5A7
1D 08H5
AC 08H5
DT 01-M
DT 01-M
DT 01-C
DE PUta
GN ONY
COC EUK

690

573 107

1 MAETVLSMARSLVGSAISKAASAAANETSLLLGVEKDIWYIKDELKTMQAFLRAAEVMKK

9

Length 1494;

168313 MW; 15BB15F247C3446B CRC64;

1494 AA;

Indels

749

325

806

606 428

371

168 DSKKRLLEMIDTNANDGPAKVICVVGMGGLGKTALSRKIFESEEDIRKNFPCNAWITV 225 : :	226 SQSFHRIELLKDMIRQLLGPSSLDQLLHELQGKVVVQVHHLSEYLIEELKERRRFV 281	282 VLDDLWILHDWNWINEIAFPKNNKKGSRIVITTRNVDLA320 : : :	321 320 340 TLYAPFEKGSQDGDSTEVGSSSTNSTTTASHILVNNKILTRMETTLAAFKEFQLIGREKE 399	321 328 : 400 KSEIIQLVTNGDGCQPEVISVCGMGGLGKTTVVRDVYQSQELRGKPEKCACVTIMRPPNC 459	329 328 329 329 329 328 328 328 328 328 328 328	VYHLDPLQMNDAISLLLRKTINIQHEDM-ESNIQMQKMVERIVNK	CGRLPLAILTIGAVLATKOVSEWEKFYEQL-PSELEINPSLEALRRWYTLGYNHLPSH	429 LKPCFLYLSIFPEDFEIQRNRLVGRWIAEGFVRPKVGMTTKDVGESYFNELINRSMI 485	486QRSRVGTAGKIKTCRIHDIIRDITVSISRQENFVLLPMGDGSDL-VQENTRHIAFHG 541	542 SMSCKTGLDWSIIRSLAIFGD-RPKSLAHAVCPDQLRMLRVLDLEDVTFLITQKD 595 : ::: : 755 NWERDQSAFESIVDMSRVRSITVFGEWKPFLSDKMRLLRVLDLEDTTGLVNH-H 808	596 FDRIALLCHLKYLSIGYSSSIYSLPRSIGKLOGLQTLAMSSTYIAALPSEISKLOCLHTL 655 :	656 RCIRELEPDNFSLMHPMKCITNTICLPKVFTPLVSRDNRAKQIABFHMAT 705 659 HAGPPTKGNYLCTRHL-LHTYGFNQLDAC-TSLCCGAATPCIMMD 911	706 KSFWSESFGVKVPKGIGKLRDLQVLBYVDIRRTSSRAIKELGGLSKLRKLAVITKGSTKR 765 	766 KCKILY-AAIEKLSSLOSLYMNAALLSDIETLECLDSISSPPDLLRTLCLNGSLEEMPNW 824	825 IEQLTHLKKFNLWSSKLKECKNMLILGALPNLMFLSLYHNSYLGEKLVFKTGAFPNL 881 :: :	882 RTLVIFNLDQLRBIRFEDGSSPQLEKIEISCCRLESGIIGIIHLPRLKEISLEYK 936	937 SKVARLGQLKGEVNTHPNREVLRMD 961 :
ර් සි	දු පු	Qy Dp	ò 8	<i>ት</i>	8 8	8 8	6 6 B	& A	& 43	ර් සි	& g	òa	ò 6	& g	& g	රු සි	à 4
QY 666 FSLNHPMKCITNTICLFKVFTPLVSRDNRAKQIAEFHWATKSFWSBSFGVKVPKGIGK 723 	Qy 724 IRDLQVLEYVDIRRTSSRAIKELGQLSKLRKLAVITKGSTKEKCKILYAAIEKLS-SLQS 782 :	OY 783 LYMNAALLSDIETLECLDSISSPPPLLRTIGLNGSLEEMPWIEQLTHLKKFNLWSS 839 : : : : : :	QY 840 KLKEGKNMLILGALPNLMFLSLYHNSYLGEKLVFKTGAPPNLRTLVI-FNLDQLREIRPE 898 	QY 899 DGSSPQLEKIEISCCRLESGIIGIIHLPRLKEISLE-YKSKVARLGQLKGEVNT 951	Qy 952 HPNRPVLRMDSDRRDHDLGAEAEGSSIEVQTADPVPDAQGSV 993 : : : : :		Q6WSR3 Q6WSR3; 05-JUL-2004 05-JUL-2004	rs rs		RP SEQUENCE FROM N.A. RX PubMed=1464721; DOI=10.1073/pnas.2435133100; RA Feuillet C., Travella S., Stein N., Albar L., Nublat A., Keller B.; RT "Map-based isolation of the leaf rust disease resistance gene Lr10	from the hexaple Proc. Natl. Acad EMBL, AY270159; GO, GO:0005524;	DR GO; GO:00428915; Fidefense response to pathogen; IEA. DR GO; GO:0042809; P:defense response to pathogen; IEA. DR InterPro; IPR00067; Disease_resist. DR InterPro; IPR001611; LRR.	INCEPTED: IPROUCHIS; NB-ARC. Pfam; PP00560; LRR 1; 2. Pfam; PP00931; NB-ĀRC; 2. PRINTS; PR00364; DISEASRRSIST. PRINTS; PR00364; DISEASRRSIST.	Duery Match 23.2%; Score 1221; DB 2; Length 1169; Dest Local Similarity 28.8%; Pred. No. 2.2e-56; Trdel 215.	1 MAETVLSMARSLVGSAISKAASAANETSLLLGVEKDIWYIKDELKTWQAFLRAAEVWKK 6	THE LINE STANDARY STANDARY SHADON STANDARY STA	120 120 119

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                                                                                                                                                                                                                                                                                                                                     563 RPKSLAHAVCPDQLRMLRVLDLBDVTFLITQKDFDRIALLCHLKYLSIGYSSSIYSLPRS
                                                                                                                           CPASL---ISP-KWRLLRVLDLED-SLNLKNEDLRHVGELHHLRYLCL-RGTEISKLP-S
                                                                                                                                                                                                  623 IGKLQGLQTLNMSSTYIAALPSEISKLQCLHTLRCIRELEFDNFSLNHPMKCITNTICLP
                                                                                                                                                                                                                                 |: |:||:: | : || |:||: |
FONLRYLETLDIQDIKVTQLPDGIAKLEKLRYL----LAGVNFSKE-----LLH
                                                                                                                                                                                                                                                                                                     683 KVFTPLVSRDNR-AKQIAEFHMATKSFWSES------FGVKVPKGIGKLRDLQVLE
                                                                                                                                                                                                                                                                                                                                                                                                      732 YVDIRRISSRAIKELGQLSKLRKLAVITKGSTKEKCKILYAAIEKLSSLQSLYMNAALLS
                                                                                                                                                                                                                                                                                                                                                                                                                                 GALPNLMFLSLYHNSYLGEKLVFKTGAFPNLRTLVI FNLDQLREIRFEDGSSPQLEKIEI
RDITVSISRQENFVLLPMGDGSDLVQENTRHIA---FHGSMSCKTGLDWSIIRSLAIFGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIETLECL-DSISSPPPLLRTLGLNGSLEEMPNWIEQLTHLKKFNLWSSKLKEGKNMLIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Keller B.;
"Analysis of a contiguous 211 kb sequence in diploid wheat (Triticum monococcum L.) reveals multiple mechanisms of genome evolution.";
Plant J. 26:307-316(2001).
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
NCBI_TaxID=4568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCCR--LES--GIIGIIHLPRLKEISLEYKSKVARLGQ-LKGEVNTHPNRP 956
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MEDLINE-21332852; PubMed=11439119;
Wicker T., Stein N., Albar L., Feuillet C., Schlagenhauf B.,
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Last sequence update)
Last annotation update)
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Triticum monococcum (Binkorn wheat) (Small spelt)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Putative resistance protein.
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Pfam; PF00931; NB-ARC; ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Bukaryota, Viridiplantes, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 23.2%; Score 1219; DB 2; Length 963; Best Local Similarity 32.8%; Pred. No. 2.1e-56; Matches 332; Conservative 210; Mismatches 347; Indels 122;
                                                                                                                                                                                                                                                                                                                                                                                                                         A Sasaki T., Mateunoto T., Katayose Y.;

Toryza sativa nipponbare(GA3) genomic DNA, chromosome 9, BAC clone:OSCHBAB0034B12.";

Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.

R EMBL, AP005735; BAD33830.1; -.

R GO; GO:0005524; F.ATP binding; IEA.

GO; GO:00042829; P:defense response to pathogen; IEA.

R GO; GO:0042829; P:defense response to pathogen; IEA.

R InterPro; IPR001611; LRR.

R InterPro; IPR001611; LRR.

R InterPro; IPR00182; MB-ARC.

R PÉam; PP00560; LRR 1; 3.

R PÉam; PP00560; LRR 1; 3.
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                                                                                                                        25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Putative resistance protein.
Name=OSJNBb0034B12.23;
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tes 353; Conserv
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                                                                                                          ------SYAEDIRNQSAR-NVDEAELVGFS 167
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                                                                                                                                                                                                                                                    SQSFHRIELLKDMIRQ----LLGPSSLDQLLHELQGKVVVQVHHLSEYLIEELKEKRYFV 281
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                                                                                                        EEVSSRNTRYNLVEPISSGTEDDMD
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                                                                                                                                                                                                                                                                                                                                                                                                                   Putative Pi-b procein.
Name=P0666G10.123;
Oryza sativa (japonica cultivar-group).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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"Oryza sativa nipponbare (GA3) genomic DNA, chromosome 8, PAC clone:P0666G10.";

L Submitted (DEC-201) to the EMBL/GenBank/DDBJ databases.

R EMBL; AP004592; BAC75861.1; -.

R Gramene; 084QL0; -.

R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:0005915; P:apoptosis; IEA.

R GO; GO:0005915; P:apoptosis; IEA.

R InterPro; IPR001611; LRR.

R InterPro; IPR001611; LRR.

R InterPro; IPR001611; LRR.

R Pfam; PF00560; LRR 1; 3.

R Pfam; PF00560; LRR 1; 3.
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1 1226 AA; 138086 MW; F45F3EBCF9F0251A CRC64;
                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                 SKVARLG------QLKGEVNTHPNRPVLRMD 961
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179 ITNDGQGGLRVIAVLETRSGPAGTVPVVRAAYQKLKGEFECHAWVRLMHSFDANQFIGSL 238
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                                                                                                                                                                           Науавака Н.,
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                             STRAIN=TONCH II-9; TISSUE-Green leaf;
MEDLINE=21582385; PubMed=11725950; DOI=10.1023/A:1012457113700;
MEDLINE=21582385; PubMed=11725950; DOI=10.1023/A:1012457113700;
Mang Z.X., Yamanouchi U., Katayose Y., Sasaki T., Yano M.;
REXPERSSION of the Pib rice-blast-resistance gene family is upregulated by environmental conditions favouring infection and by chemical signals that trigger secondary plant defences.";
Plant Mol. Biol. 47.653-661(2001).
EMBL; AB013451; BAA93618.1;
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: 1226 AA; 138086 MW; F45F3EBCF9F0251A CRC64;
                                                                                                                                                                                                    "The Pib gene for rice blast resistance belongs to the binding and leucine-rich repeat class of plant disease genes.";
                                                                                                                              STRAIN=Tohoku IL-9; TISSUE-Green leaf;
MEDLINES-99348180; PubMed=10417726;
Wang Z., Yano M., Yamanouchi U., Iwamoto M., Monna L.,
Katayose Y., Sasaki T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 27.5%; Pred. No. 4.5e-56; Matches 353; Conservative 196; Mismatches 349;
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                                                                 NCBI_TaxID=4530;
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    VSQPVNSDSTKWKSETRSSMEGASTTSDSKTVPSDGVIQEDGPKDLPESSLPPHLNRDSN 418
                                                                                                                                                                                                                      ----SEYLIEBLKE----KRYFVVLDDLWILHDWNWINEIAFPKNNKKGSRIVITTRNVD 318
                                                                                                                                                                                                                                               LAEKCATASL-VYHLDFLOMNDAISLLLRKTINKNHEDMESNKNMOKMVERIVNKCGRLPL 377
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                                                                                                                                                             -- AKVICVVGMGGLGKTALSRKIFESEE
                                                                                                                                  212 DIRKNFPCNAWITVSQSFHRIELLKDMIRQLLGPSSLDQLLHELQGKVVVQVHHL----
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01-OCT-2000 (TrEMBLrel. 15, L
01-MAR-2004 (TrEMBLrel. 26, L
PibH8 protein.
Name=PibH8;
Oryza sativa (Rice).
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RT "Oryza gativa nipponbare (GA3) genomic DNA, chromosome 8, PAC RT clone:P0666G10."; RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. DR EMBL; AP004592; BAD3147.1; DR GO; GO:0005524; F:ATP binding; IEA. DR GO; GO:000524; F:ATP binding; IEA. DR GO; GO:00042829; Pedfense response to pathogen; IEA. DR GO; GO:00042829; Pedfense response to pathogen; IEA. DR InterPro; IPR001611; LRR. DR InterPro; IPR001611; LRR. DR PEAM; PR00560; LRR 1, 2. DR PEAM; PR00560; LRR 1, 2. DR PEAM; PR00560; LURR 1, 2. DR PEAM; PR00186; SUBTILASEASESIST. DR PROSITE; PS00136; SUBTILASE ASP; UNKNOWN 1. SQ SEQUENCE 1485 AA, 167594 AW; 181AB0967BAB8006 CRC64;	Query Match 22.8%; Score 1199; DB 2; Length 1485; Best Local Similarity 24.9%; Pred. No. 4.5e-55; Matches 380; Conservative 194; Mismatches 345; Indels 606; Gaps 33; Qy I MAETVLSMARSLVGSARSAAANNETSLLIGVEKDIWIKDELKTMQAFLRAAEVMKK 60		146181 DGDGLQEIAVWGTSGATGVASVVMVAYQKVKDRFPECHAWVKVMHPFDAKEFIGSLVRQF	Db 241 KANSHEGTSNTPQGTPSGVSALNEMBAKDYNLLDDFCKYVANKKYLIALNGLCNIEEWDW 300 Qy 146YAEDIRN 152 Db 301 IKTYLPNKHNGSRILVCTPQAEVAICWKNKDGYKVSBIRQEGSFVTPLYVFYEEVKDSPT 360 Qy 153	QY 153	29 158
Db 479 LEKLGFERRAWVTULREFQLTELERSLAQRLVKDSPCKKVESIPGLARSGL 529 Qy 267SEXLIEELKE	Qy 436 LSIFPEDFEIQRNRLVGRWIAEGEVRPKVGMTTKDVGESYFNELINRSMIQRSRVGTAGK 495	Db 768 TGFCQVYNLAMELIISKSEENLVLVLDDHITSRSKDRVRHLVVSKSMSRENDMQNIVD 827 Qy 551 WSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLEDVTFLITQKDFDRIALLCHLKYLSI 610 Db 828 VSHIRSLTVFGEW KSFFLSKKORMLRVLDLEDAEGL-QDPDLVPIGKLHHLKYLSI 882 Qy 611 GYSSIYSLPRSIGKLGGLGTLNRSTYIAALPSEISKLQ	651 CLHTLRCIRELEFDNFSLNHPMKCITNTICLPKVFTPLVSRDNRAKQIAEFHMATKSFWS	Db 972 RNLDVCGVKVPRGIGRLRSIHTLSIVNIAR-GKALLKNLKKLTQLCKLGVTGINKNNC 1028 Qy 768 KILYAAIEKLSSLQSLYMNAALLSDIETLECLDSISSPPPLLRTLGLNGSLEEMPNWIEQ 827	Qy 888 NLDQLREIRFEDGSSPQLEKIEISCCRLESGIIGIIHLPRLKEISL	RESULT 11 069U98 ID 069U98 DG 50U98 To 069U98 To 069U98 To 125-OCT-2004 (TrEMBLrel. 28, Last sequence update) DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update) CN Name=P0666G10.130; CN CEL Annotation (TremBlrel. 28, Last annotation). CN CEL TaxID=39947; RN 1] RP SEQUENCE FROM N.A. RA Sasaki T., Matsumoto T., Yamamoto K.;

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Kamihara

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61 NSKVVKTWVKQVRDTAYDVEDSLQDFAVHLKRPSWMRFPRTLLERHRVAKQMKELRNKVE 120
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DVSQRNVRYHLIKGSAKATINSTEQ--SSVIATAIFGIDDARRAAKQDNQRVDLVQLI--
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                                                           SEQUENCE FROM N.A.
STRAIN=BL-1; TISSUE-Green leaves;
JWA N., Tsunoda Y., Akiyama K., Nakamura S., Motomura T.
Kodama O., Kawasaki S.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                      pathogen; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22.7%; Score 1191; DB 2; 27.7%; Pred. No. 9.4e-55; ive 208; Mismatches 363;
                                                                                                                                                                 EMBL; AB011449; BAA76282.2; ...
EMBL; AB0113449; BAA76281.2; ...
GRAMEI, AB026839; BAA85975.1; ...
Gramene; Q9SSY0; ...
Gramene; Q9SNV6; ...
GO; G0:0005524; F:ATP binding; IEA.
GO; G0:0006515; P:ATP binding; IEA.
GO; G0:0006915; P:ATP binding; IEA.
GO; G0:0006915; P:ATP binding; IEA.
                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000767; Disease_resist.
InterPro; IPR001611; LRR.
InterPro; IPR002182; NB-ARC.
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Pfam; PF00931; NB-ARC;
                      Plant J. 19:55-64(1999)
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Best Local Similarity
Matches 355; Conserv
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                                                                                                                                                         888 KKCGRLPLAIVAVGGFLSTRPPNIREWRKFSDHISTELDENPSLEMIKKILISSYEGLSY 947
                                                                                                                                                                                                                                                                                                    SRVGTAGKIKTCRIHDIIRDITVSISRQENFVLLPMGDGSDLVQENTRHIAFHGSMS--- 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----ESFGVKVPKGIGKLRDLQVLEYVDIRRTSSRAIKELGQLSKLRKLAVITKGST 763
                                            331 H-LDFLQMNDAISLLLRK------TNKOHED------MESNKOMQKAVERIV 369
                                                                                                                                370 NKCGRLPLAILTIGAVLATK--QVSEWEKFYEQLPSELEINPSLEALRRMVTLGYNHLPS 427
                                                                                                                                                                                                                  HLKPCFLYLSIFPEDFEIQRNRLVGRWIAEGFVRPKVGMTTKDVGESYFNELINRSMIQR 487
KQDLTGKKYLIVLDDLSTTTEWDFIKTI-PPENS--SSRIIVTTRPKLVAQHCSEEEEYM
                                                                      ALLCHIKYLSIGYSSSIYSLPRSIGKLOGLOTLNMSSTYIAALPSEISKLOCLHTLRC--
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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resistance
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MEDLINE=99348180; PubMed=10417726;
Wang Z., Yano M., Yamanouchi U., Iwamoto M., Monna L., Hayasaka Katayose Y., Sasaki T.;
"The Pib gene for rice blast resistance belongs to the nucleotid binding and leucine-rich repeat class of plant disease resistance
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=PIB; Synonyms=Pi-b;
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COSUNG
DD 01-MA
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DT 01-MA
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DB Pib.
DB Pib.
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Length 1251;

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Gape

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203 234

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EEDIRKNPPCNAWITVSQSFHRIELLKDMIRQLLGPS------SLDQLLHELQ 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NVDLAEKCAT--ASLVYHLDFLQMNDAISLLLRKT--NKNHEDMESNKMMQKMVERIVNK 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LKPCFLYLSIFPEDFEIQRNRLVGRWIAEGFVRPKVGMTTKDVGESYFNELINRSMIQRS 488
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                                                                                                                                                                                                                                                                                        Query Match 22.4%; Score 1174.5; DB 2; Length 1011; Best Local Similarity 31.1%; Pred. No. 5.3e-54; Matches 334; Conservative 197; Mismatches 365; Indels 179;
                                                                                                                                                                                                                         PRINTS; PRO0364; DISEASERSIST.
PROSITE; PS00053; RIBOSOMAL S8; UNKNOWN 1.
SEQUENCE 1011 AA; 114012 WW; 14EDDBBA31A4835C CRC64;
                     сргомовоме
                                                                                                                pathogen; IEA
                     rice
 Yano M., Jiang J., Gojobori T.;
"The genome sequence and structure of ric
Mature 420:312-316(2002).
EMBL; AP001073; BAA89580.1; -.
Gramene; O9LJ10; -.
Gramene; O9LJ10; -.
GO; CO:0005524; F:AFF binding; IEA.
GO; GO:0006915; P:APF binding; IEA.
GO; GO:0006915; P:APF binding; IEA.
GO; GO:00042829; P:Gefense response to pat
InterPro; IPR001611; LRR.
InterPro; IPR001611; LRR.
                                                                                                                                                                                          Pfam; PF00560; LRR 1; ; Pfam; PF00931; NB-ARC;
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PubMed=1244438; DOI=10.1038/nature01184;
Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
A Wu J., Nimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamoti H.,
A Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
A Hijishita S., Honda M., Ichikawa Y., Idohuwa Y., Iijima M., Ikeda M.,
A Karasawa W., Katagiri S., Kkuta A., Kobayashi N., Kono I.,
A Karasawa W., Katagiri S., Kkuta A., Kobayashi N., Kono I.,
Andrita K., Machara T., Mizuno H., Mizubayashi T., Mukai Y.,
Nachita K., Machara T., Mizuno H., Mizubayashi T., Makamura M.,
A Marasawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
Bhimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
A Rhim K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukwa K.,
Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
                                                                                                                                                                                                                                                                                                                                                                                       : | : ::::| |: | || | | | : : || |: || |: || |: || |: || :::| |: || .::| |: || VGR-GNAILRDIGMLTGLHKLGV--AGINKKNGRAFRLAISNLNKLESLSVSSAGMPGL- 1052
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---HKA-----LARRDAWTFACCVKFPSIMTGVHEEEGAMVPSGIRKLKDLHTLRNIN
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                                                 TKDVGESYFNELINRSMI --- QRSRVGTAGK-IKTCRIHDIIRDITVSISRQENFVLLPM
                                                                                                                GDGSDLVQENTRHIA----FHGSMSCKTGL-DWSIIRSLAIFGDRPKSLAHAVCPDQLRM
                                                                                                                                            EGCSAYIHGAIRHLAISSNWKGDKSEFEGIVDLSRIRSLSLFGDWKPFFVYG----KMRF
                                                                                                                                                                           LRVLDLEDVTFLITQKDFDRIALLCHLKYLSIGYSSSIYSLPRSIGKLQGLQTLNMSSTY
                                                                                                                                                                                                                                          IAALPSEISKLOCLHTLRCIRELEF---DNFSLNHPMK---CITNTICLP---KVFTPLV
                                                                                                                                                                                                                                                                                                        SRDNRAKQIAEFHWATKSFWS------ESFGVKVPKGIGKLRDLOVLEYVD
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 16, Last sequence update)
01-OKT-2004 (TrEMBLrel. 26, Last sequence update)
Similar to Oryza sativa gene for Pib.
Oryza sativa (japonica cultivar-group).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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1229 KGGELKRKIREQLARNPNQPII 1250
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                                                                                                                                  340 A----ISLLLRKTNKNHEDMESNKNMQ-KMVERIVNKCGRLPLAILTIGAVLATKQVS
                                                                                                                                                                                                                                                                                                                                                                                              431 DRWLAEGLVRDRTGMSPRTVAKWYLLWLIDRSMIMVSNLRKNRSFKTCWIHPMMRDILVM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VVLDDLWILHDWNWINEIAFPKNNKKGSRIVITTRNVDLAEKCATA-SLVYHLDFLQMND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       512 ISROENF-VLLPMGDGSDLVQENTRHIAFHGSMSCKTG--LDWSIIRSLAIFGDRPKSLA
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                            331 SFERFKALILVTENSKMTHEDREDFEDLDLKELDRL-------
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Sasaki T., Matsumoto T., Yamamoto K.;
"Oryas sativa nipponbare(GA3) genomic DNA, chromosome 6, clone:PPO/02POS.";
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005828; BAD46437.1; -.
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to NBS-LRR type resistance gene.
DVNVTKVFKDMMKQLFDDSSSQPEYTGEDELAHGIQ-
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                                                                                                 ---IPPGLSAMESLÓTIAHANV-TSSGI
                                                                                                                                                                AIKBIGOLSKIRKLAVITKGSTKEKCKILYAAIEKLS-SLOSLYMNAALLSDIETLECLD
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative NBS-LRR type resistance gene.
Name=071449_H02.21;
Oryza sativa (japonica cultivar-group).
Grza sativa (japonica cultivar-group).
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sasaki T., Matsumoto T., Yamamoto K.; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AP004648; BADD1287.1; GO; GO:0005524; F:ATP binding; IEA. GO; GO:0005915; P:apoptosis; IEA. GO; GO:0042829; P:defense response to pathogen; IEA. InterPro; IPR000767; Disease resist.
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884 AA; 101271 MW; 3D03F1A1FC00BF3A CRC64;
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PF00931; NB-ARC; 1
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                              -----RHRIAIRIHNLKSRVEEVSSRNTRY--NLVEPISSGTEDDMDSYAEDIRNQSA 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               260 VVQVHHLSE------YLIBELKEKRYFVVLDDLWILHDWNWINBIAFPKNNKKG 307
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                                                                                                                        Gaps
                                                         Query Match 21.9%; Score 1152.5; DB 2; Length 989; Best Local Similarity 31.3%; Pred. No. 7.6e-53; Matches 325; Conservative 186; Mismatches 383; Indels 143;
989 AA; 109590 MW; 09BF11AAD9C3028A CRC64;
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Qy 940 ARLGQLKGEVNTHPNRP 956 : :: | | | | | | Db 959 SVVSKVVSCVKDHPNHP 975 Search completed: February 9, 2005, 08:47:40 Job time: 137.377 secs

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February 9, 2005, 08:53:28; Search time 94.0327 Seconds (without alignments) 3574.555 Million cell updates/sec
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5255
1 MAETVLSMARSLVGSAISKA.....SQVITLTINDSEBIGTAQAG 1032
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 89, Appl	Sequence 93, Appl	Sequence 139799,	Sequence 104966,	Sequence 143499,	Sequence 85, Appl		Sequence 87, Appl	Sequence 110261,	Sequence 151916,	Sequence 91, Appl		Sequence 177336,
, OI	US-10-352-179-89	US-10-352-179-93	US-10-437-963-139799	US-10-437-963-104966	US-10-437-963-143499	US-10-352-179-85	US-10-437-963-141086	US-10-352-179-87	US-10-437-963-110261	US-10-437-963-151916	US-10-352-179-91	US-10-437-963-171923	US-10-437-963-177336
	15	15	16	16	16	15	16	15	16	16	15	16	16
% Query Match Length DB	1031	1091	1531	993	974	979	862	993	1001	1163	1054	926	812
& Query Match	95.1	94.5	80.1	69.2	58.2	58.1	53.6	49.4	48.2	47.3	46.2	36.2	36.1
Score	4997	4966.5	4209.5	3636	3060.5	3055.5	2819	2595	2532	2483.5	2427	1903	1894.5
Result No.	-	8	m	4	S	9	7	80	6	10	11	12	11

Sequence 95, Appl Sequence 197236,		Sequence 149303,			Sequence 190992, Sequence 190783,			Sequence 125137,	Sequence 170107,	Sequence 36, Appl	Sequence 36, Appl	Sequence 181404,		Sequence 120373,					Sequence 181820,			Sequence 172739,		13726	٠.	19015	Sequence 174758,
US-10-352 US-10-437	US-10-437-963-1	US-10-437-	US-10-437-963-	US-10-437-	US-10-43/-963-190992 US-10-437-963-190783	US-10-437-	ns-		ns-	ns-0	US-10-267-	ns-	ns-		ns-	ns-	US-10-437-963-	US-10-437-963-	US-10-437-963-	US-10-437-963-	US-10-437-963-2	US-10-437-963-1	US-10	US-10-437-963-			US-10-437-963-174758
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ALIGNMENTS

RESULT 1 US-10-352-179-89 US-10-352-179-89 PROPLICATION NO APPLICANT: Wa APPLICANT: Wa TITLE OF INVER FILE REFERENC CURRENT FILING PRIOR PILING PRIOR PILING PRIOR PILING PRIOR PILING OUNDBER OF SEG SOFTWARE: PAL SEG ID NO 89 LENGTH: 1031 LENGTH: 1031 TYPE: PRT TYPE: PRT	SULT 1 -10-352-179-89 Sequence 89, Application US/10352179 Sequence 89, Application US/10352179 Sequence 89, Application US/10352179 Sequence 89, Application US/10352179 Sequence 80, Application US/10352179 GENERAL INFORMATION: APPLICANT: Wang, Guo-liang APPLICANT: Liu, Guiff TILE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Planting PILING DATE: 2027/04108 CURRENT APPLICATION NUMBER: 60/352,106 FRIOR FILING DATE: 2002-01-25 FRIOR FILING DATE: 2002-01-25 NUMBER OF SEQ ID NOS: 97 SOFTWARE: Patentin version 3.1 SEQ ID NO 89 LENGTH: 1031 TYPE: PRT ORGANISM: Oryza minuta ORGANISM: Oryza minuta
Query Match	Query Match 95.1%; Score 4997; DB 15; Length 1031;
Best Local	Best Local Similarity 96.4%; Pred. No. 0;
Matches 98	Matches 985; Conservative 12; Mismatches 25; Indels 0; Gaps 0;
oy	1 MAETVLSMARSLVGSAISKAASAANETSLLLGVEKDIWYIKDELKTMQAFLRAAEVMKK 60
Pp	
oy	61 KDELLKVWARQIRDLSYDIEDSLDEFKVHIESQTLFRQLVKLRERHRIAIRIHNLKSRVB 120
Ob	
Oy 12	121 BVSSRNTRYNLVEPISSGTEDDMDSYAEDIRNQSARNVDEAELVGFSDSKKRLLEMIDTN 180
Db 12	

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YNHLPSHLKPCFLYLSIFPEDFEIQRNRLVGRWIAEGFVRPKVGMTTKDVGESYFNELIN 481
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                                                                                                                                         MAETVLSMARSLVGSAISKAASAAANETSLLLGVEKDIW
                                                                                                 94.5%; Score 4966.5; llarity 90.4%; Pred. No. 0; Conservative 20; Mismatches
PRIOR APPLICATION NUMBER: 60/352,106
PRIOR FILING DATE: 2002-01-25
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn version 3.1
SEQ ID NO 93
LENGTH: 1091
                                                          ; TYPE: PRT
; ORGANISM: Oryza minuta
US-10-352-179-93
                                                                                               Query Match
Best Local Similarity
Matches 986; Conserv
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APPLICANT: Wang, Guo-liang
APPLICANT: Liu, Guifu
TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in
FILE REFERENCE: 22777/04108
CURRENT APPLICATION NUMBER: US/10/352,179
CURRENT FILING DATE: 2003-01-27
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                       ANDGPAKVICVVGMGGLGKTALSRKIFESEEDIRKNPPCIAWITVSQSFHRIELLKDMIR 240
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                                                 QLLGPSSLDQLLHELQCKVVVQVHHLSEXLIEELKEKRYFVVLDDLWILHDWNWINEIAF
                                                            GSMSCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLEDVTFLITQKDFDRIA
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Sequence 93, Application US/103:
Publication No. US2004000678BA1
GENERAL INFORMATION:
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Shou, Yibua
APPLICANT: Shou, Yibua
APPLICANT: Cao, Yongwei
APPLICANT: Wei
APPLICANT: Wei
APPLICANT: Buokharov, Andrey A.
APPLICANT: Buokharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REFERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEG ID NOS: 204966
SEQ ID NO 104966
SEQ ID NO 104966
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493 AGKIKTCRIHDIIRDITVSISRQENFVLLPMGDGSDLVQENTRHIAFHGSMSCKTGLDWS
                            AGKIKTCRIHDIIRDIIVSISRQENFVLLPMGDGSDLVQENTRHIAFHGSMSCKTGLDWS
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                                                                                                                                          IIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLEDVTFLITQKDFDHIALLCHLKYLSIGY
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US-10-437-963-104966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 104966, Application US/10437963; Publication No. US20040123343A1; GENERAL INFORMATION:
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ORGANISM: Oryza sativa
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80.1%; Score 4209.5; DB 16; Length 1531;
Best Local Similarity 92.6%; Pred. No. 7.4e-305;
Matches 829; Conservative 21; Mismatches 42; Indels 3; (
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US-10-437-963-139799
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                                                                                              PKNNKKGSRIVITTRNVDLAEKCATASLVYHLDFLOMNDAISLLLRKTNKNHEDMESNKN 360
MQKMVERIVNKCGRLPLAILTIGAVLATKQVSEWEKFYEQLPSELEINPSLEALRRWVTL
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                          ANDGPAKVICVVGMGGLGKTALSRKIFESEEDIRKNFPCNAWITVSQSFHRIELLKDMIR
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RMEEDRSCHDLRRDGKGSAVE
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US-10-437-963-143499
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Sequence 143499, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei

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APPLICANT: Boukharov, Andrey A. APPLICANT: Boukharov, Andrey A. APPLICANT: Barbazuk, Brad APPLICANT: Li, Ping APPLICANT: Li, Ping TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 143499
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Best Local Similarity 62.8%; Pred. No. 2.5e-219;
Matches 610; Conservative 141; Mismatches 217; Indels
                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT4530_44401C.1.pep
US-10-437-963-143499
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GENERAL INFOGRATION:
CARDITCANT: LA ROBA:
APPLICANT: LA ROBA:
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Wei
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APPLICANT: Wei
APPLICANT: Wei
APPLICANT: Bachbaruk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 141086
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                                     INRSMIQRSRVGTAGKIKTCRIHDIIRDITVSISRQENFVLLPMGDGSDLVQENTRHIAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT4530_42224C.1.pep
US-10-437-963-141086
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; Publication No. US20040123343A1
; GENERAL INFORMATION:
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Publication No. US20040006788A1
GENERAL INFORMATION:
APPLICANT: Wang, Guo-liang
APPLICANT: Liu, Guifu
APPLICANT: Liu, Guifu
TITLE NFERENCE: 22727/04108
CURRENT FILING DATE: 2003-01-27
PRIOR PRINCA APPLICATION NUMBER: 05/10/352,106
PRIOR FILING DATE: 2002-01-25
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SOFTWARE: Patentin version 3.1
SEQ ID NO 85
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; ORGANISM: Oryza minuta
US-10-352-179-85
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US-10-352-179-85
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                            EVSSRNTRYNLVE-PISSGTEDDMDSYAEDIRNQSARNVDEAELVGFSDSKKRLLEMIDT 179
                                    NANDGPAKVICVVGMGGLGKTALSRKIFESEEDIRKNFPCNAWITVSQSFHRIELLKDMI 239
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RESULT 8
US-10-352-179-87
US-10-352-179-87
; Sequence 87, Application US/10352179
; Publication No. US20040006788A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Guo-liang
; APPLICANT: Liu, Guifu

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OF INVENTION: Procedures and Materials for Conferring Disease Resistance
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                                                                                                                                                      Query Match 49.4%; Score 2595; DB 15; Best Local Similarity 55.3%; Pred. No. 1.6e-184; Matches 539; Conservative 164; Mismatches 242;
        FILE REFERENCE: 22727/04108
CURRENT APPLICATION NUMBER: US/10/352,179
CURRENT APPLICATION NUMBER: US/10.27
PRIOR APPLICATION NUMBER: 60/352,106
PRIOR FILING DATE: 2002-01-25
NUMBER: OF SEQ ID NOS: 97
SEQ ID NO 87
                                                                                                           ; TYPE: PRT
; ORGANISM: Oryza minuta
US-10-352-179-87
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APPLICANT: LA ROSA, Thomas J.
APPLICANT: LA ROSA, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thou Y Willian
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei, Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
FEQURENT 11:016
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                     415 VTLSYGHLPSHLKPCYLYLSIFPEDIEIKRRHLVNRWVAEGLVRARVGMTISDVGESYFD
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                                                                                                                                                538 AFHGSMSCKTGLDWSIIRSLAIFGD---RPKSLAHAVCPDQLRMLRVLDLEDVTFLITQK
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US-10-437-963-151916
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; Publication No. US20040123343A1
; GENERAL INFORMATION:
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ORGANISM: Oryza sativa
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Sono, Yihua
APPLICANT: Sono, Yihua
APPLICANT: Sono, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53221)B
CURRENT FILLING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 110261
LENGTH: 1007
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                                                                                                           ANDGP-AKVICVVGMGGLGKTALSRKIFESEEDIRKNFPCNAWITVSQSFHRIELLKDMI 239
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                 LWSSKLKEGKNMLILGALPNLMFLSLYHNSYLGEKLVFKTGAFPNLRTLVIFNLDQLREI
                                                                                        RFEDGSSPQLEKIEISCCRLESGIIGIIHLPRLKEISLEYKSKVARLGQLKGEVNTHPNR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Clone ID: PAT_MRT4530_14340C.1.pep
                                  Sequence 110261, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
                                                                                                                                                             PVLRMDSDRRDHDLG 970
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PMLRLFGERSRHDLG 950
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                          RESULT 9
US-10-437-963-110261
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US-10-437-963-110261
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                                                                                EAELVGFSDSKKRLLEMIDTNANDGPAKVICVVGMGGLGKTALSRKIFESEEDIRKNFPC 219
                                                                                                                        NAWITVSQSFHRIELLKDMIRQLLGPSSLDQLLHELQGKVVVQVHHLSEYLIEELKEKRY 279
                                                                                                                                                                                            FVVLDDLWILHDWNWINBIAFPKNNKKGSRIVITTRNVDLAEKCATASLVYHLDFLQMND 339
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                              YIKDELKTWOAFLRAAEVMKKKDELLKVWAEQIRDLSYDIEDSLDEPKVHIESQTLFROL
            Gaps
            37;
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al Similarity 52.9%; Pred. No. 4.2e-176; 521; Conservative 163; Mismatches 263;
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                                                                                                                                                                                                          Length 1054;
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                                                                                                                                                                                                          Query Match 46.2%; Score 2427; DB 15; Best Local Similarity 51.9%; Pred. No. 6.1e-172; Matches 530; Conservative 144; Mismatches 261;
                                                     for
                                                     and Materials
                            APPLICANT: Wang, Guo-liang
APPLICANT: Liu, Guifu
TITLE OF INVENTION: Procedures and Materials
TITLE PERERNCE: 22727/04108
CURRENT FILING DATE: 2003-01-27
PRIOR APPLICATION NUMBER: 60/352,179
PRIOR PILING DATE: 2002-01-25
NUMBER: OF SEQ ID NOS: 97
SEQ ID NO 91
 US/10352179
Sequence 91, Application US/103 Publication No. US20040006788A1 GENERAL INFORMATION:
                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Oryza minuta
US-10-352-179-91
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Xovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
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; Publication No. US20040123343A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lances, Thomas J.
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION UNMERS: US/10/437,963
TITLE REPERENCE: 38-21/63221)B
TITLE OF INVENTION UNMERS: US/10/437,963
TITLE US THENDER OF SEQ ID NOS: 204966
TENTH: 226
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| |-----| |-----| |-----| |-----| |----| |----| |----| |----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----| 
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                                                                                                                                                                                                              756 HKGKMDTLYSYPE-----ALPPTISPCECCGEFRYWNTSVYRFYFISSSPTED
                                                                                                                                                                                                                                                                                         807 - PLLRTLGLNGSLEEMPNWIEQLTHLKKFNLWSSKLKEGKNWLILGALPNLMPLSLYHNS
                                                                                                                                                                                                                                                                                                                                                                         804 TQVERKSGDALDAAHAPDEVQ-----LMEEQTKRRNHVGTCGVAQPHGPLSSFQCL
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US-10-437-963-171923
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OTHER INFORMATION: unsure at all Xaa locations
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TYPE: PRT
ORGANISM: Oryza minuta
US-10-352-179-95
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                                                                                                                                                                                                                                                                                                                                            SFHRIELLKDMIRQLLGPSSLDQLLHELQGKVVVQVHHLSEYLIEELKEKRYF-VVLDDL 286
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                                                                                                                                                                                                                  29 IAIRIHNIKSRVEEVSSRNTRYNLVEPISSGTEDDMDSYAEDIRNQSARNVDEAELVGFS
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  for Plant Improvement
                                                                                                                                                    Query Match 36.1%; Score 1894.5; DB 16; Length 812; Best Local Similarity 45.5%; Pred. No. 2.4e-132; Matches 453; Conservative 87; Mismatches 191; Indels 265;
                                                                                                                  ; OTHER INFORMATION: Clone ID: PAT_MRT4530_74999C.1.pep
US-10-437-963-177336
TITLE OF INVENTION: Plants and Uses Thereof
FILE REFERENCE: 38-21(53221) B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 177336
                                                                                 TYPE: PRT
ORGANISM: Oryza sativa
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RESULT 14

US-10-352-179-95

US-10-352-179-95

Sequence 95, Application US/10352179

Publication No. US20040006788A1

GENERAL INFORMATION:

APPLICANT: Wang, Guo-liang

APPLICANT: Liu, Guifu

TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pla

FILE REFERENCE: 22727/04108

FILE REFERENCE: 22727/04108

CURRENT APPLICATION NUMBER: US/10/352,179

CURRENT APPLICATION NUMBER: 60/352,106

PRIOR APPLICATION NUMBER: 60/352,106

NUMBER OF SEQ ID NOS: 97

NUMBER OF SEQ ID NOS: 97

SOFTWARE: Patentin version 3.1
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                                                                                                                             THLKKFNLWSSKLKEGKNMLILGALPNLMFLSLYHNSYLGEKLVFKTGAFPNLRTLVIFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KDELLKVWAEQIRDLSYDIEDSLDEFKVH1ESQTLFRQLVKLRERHRIAIRIHNLKSRVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 QLLGPSSLDQLLHELQGKVVVQVHHLSEYLIEELKEKRYFVVLDDLWILHDWNWINEIAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GYNHLPSHLKPCFLYLSIFPEDFEIQRNRLVGRWIAEGFVRPKVGMTTKDVGESYFNELI
                                              638 KHLVKIYLYKSHL-NGDTMEILGELHNLMDLHFRWYAYVGEKLVFIEGAFQNLRKLVVET
                                                                                                     LDQLREIRFEDGSSPQLEKIEISCCRLESGIIGIIHLPRLKEISLEYKSKVARLGQLKGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAETVLSMARSLVGSAISKAASAANETSLLLGVEKDIWYIKDELKTMQAFLRAAEVMKK
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634

683

989 743

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687 TLADVVCRCRRG--FSECCESSSSCFAGHFSVRAPEGIEKLRNLHMLGVVRIERDSGVA- 743
                                                                                                                                                                                                                                                                                 744 KELGQLSKLRKLAVITKGSTKEKCKILYAAIBKLSSLQSLYMNAALLSDIBTLECLDSIS 803
                                                                                                                                                                                                                                                                                                     804 SPPPLLRTLGLNGSLEEMPNWIEQLTHLKKFNLWSSKLKEGKNMLILGALPNLMFLSLYH 863
                                                                                                                                                                                                                                                                                                                                                                                        799 - APKHLLSLRLYGHLEKLPDWVSSLNDLAKVKLLETQL-EQKDINLLGNLSNLTSLGLWG 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                 635 SSTYIAALPSBISKLOCLHTLRCIRBLEFDNF-----SLNHPMKCITNTICLPK
519 VLLPMGDGSDLVQENTRHIAF----HGSMSCKTGLDWSIIRSLAIFGDRPKSLAHAVCPD
                                                                   575 QLRMLRVLDLEDVTFLITQKDFDRIALLCHLKYLSIGYSSSIYSLPRSIGKLQGLQTLNM
                                                                                                                                                                        635 ODTKVTHLPDGTAKLEKLRYL----LAGINFAEDLAEKMOTNAKNKVNKCNGN---LLE
                                                                                                                                                                                                           684 VFTPLVSRDNRAKQIAEFHMATKSFWSESFGVKVPKGIGKLRDLQVLEYVDIRRTSSRAI
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ne : 99.0327 secs
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                                                                                                                                Sequence 197256, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Acoult, David K.

APPLICANT: Acoult, David K.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Brad

APPLICANT: Boukharov, Brad

APPLICANT: Boukharov, Para

APPLICANT: Boukharov, Para

APPLICANT: Boukharov, Para

APPLICANT: Boukharov, Brad

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF PREPRENCE: 38-21(53221)8

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 AGDTARTWVKQVRDLAYDVEDCLLDFALHAHAHASSSSCAPPLWIRPWRLAERHRVAARI 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LPSELEINPSLEALRRWYILGYNHLPSHLKPCFLYLSIFPEDFEIQRNRLVGRWIAEGFV 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 KDELLKVWAEQIRDLSYDIEDSLDEFKVHIESOT-----LFROLVKLRERHRIAIRI 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 HNLKSRVEEVSSRNTRYNLVEPISSGTEDDMDSYAEDIRNQSARNVD-----EAELVGF 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDSKKRLLEMIDTNANDGP---AKVICVVGMGGLGKTALSRKIFESEEDIRKNFPCNAMI 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            224 TVSQSFHRIELLKDMIRQLLGPSSLDQLLHELQGKVVVQVHHLSEYLIEELKEKRYFVVL 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DDLWILHDWNWINEIAFPKNNKKGSRIVITTRNVDLAEKCATA-SLVYHLDFLQMNDAIS 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LILERTINKNHEDMESNKNMOKMVERIVNKCGRLPLAILTIGAVLAT--KOVSEWEKFYEQ 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAETVLSMARSLVGSAISKAASAAANETSLLLGVEKDIWYIKDELKTMQAFLRAAEVMKK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90; Gaps
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23.3%; Score 1224; DB 16; Length 978;
Best Local Similarity 32.8%; Pred. No. 4e-82;
Matches 330; Conservative 209; Mismatches 377; Indels 90.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: PAT_MRT4530_93011C.1.pep
US-10-437-963-197236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Oryza Bativa
                545
                                               443 GSKYC 447
                                                                                                                     US-10-437-963-197236
                GSMSC
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 197236
LENGTH: 978
                541
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Sasaki, T., Matsumoto, T. and Katayose, Y.

Direct Submission
Submitted (21-Aug-2002) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program; Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)
On Apr 8, 2004 this sequence version replaced gi:22415844.
The orientation of the sequence is from SP6 to T7 of the PAC clone.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .138870

/organiam-Oryza aztiva (japonica cultivar-group) '

/oul_type="ganomic DNA"

/cultivar="Nipponbare"

/db_xref="taxon:39947"

/chromosome="96"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 8; Length 138870;
AK103886

AP003862

AP003862

AC109832

AC109832

AC109832

AC11308

AC121327

AC131317

AC1313117

AC137924

AC1379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sasaki,T., Matsumoto,T. and Katayose,Y.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome clone:P0649C11
Dublished Only in Database (2002)
2 (bases 1 to 138870)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
genomic DNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 2843.4;
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                                                           AC109812
AK101707
AK005775
CNS07878
AK01323176
AK119293
AC11247
CNS07708
AC124968
AC124968
AC124968
AC124968
                                                                                                                                                                                                                                                         AK066020
AC120530
AC130924
AC146948
AF114171
AC138002
AK103311
AK066779
AK064730
AK06473
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Best Local Similarity
Matches 2901; Conserv
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179.2
178.6
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150.4
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AP005659
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
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   ORIGIN
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AK121397 Oryza sat
AF020494 Hordeum v
AK120452 Oryza sat
AP001168 Oryza sat
AK070885 Oryza sat
AK071029 Oryza sat
AK071029 Oryza sat
AK073612 Oryza sat
AK073612 Oryza sat
AK073612 Oryza sat
AK073612 Oryza sat
AK065693 Oryza sat
                                                                                                            ; Search time 8745.62 Seconds (without alignments) 17170.053 Million cell updates/sec
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                                                                                                                                                                                                            1 atggcggagacggtgctgag......gcacagctcaagctggctga 3099
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                5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4708233 segs, 24227607955 residues
                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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                GenCore version
Copyright (c) 1993 - 2005
                                                                                                             22:05:35
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Maximum Match 100%
Listing first 45 summaries
                                                                               sw model
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AK070885
AK071029
HWU506137
AK101823
AK073612
AB013451
AK065693
AF065693
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HVU507094
AK120452
AP003487
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AK065372
AC114983
                                                                                                                                                                                                                                        IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                             2005,
                                                                             nucleic search, using
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length: 2000000000
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3099
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Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.8 138870
51.4 3890
48.6 122193
48.6 122193
41.5 3457
38.9 4326
35.6 176979
16.8 2015
7.0 4949
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FLI_CDNA; CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyea; Liliopsida; Poales; Poaceae;
Enrhartoideae; Oryzeae; Oryza.
37526 CAAACGGGTCGACAAAGGAAAATGTAAGATACTTTATGCAGCCATTGAGAAGCTCTCTT 37585
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                                                                     GGAGCAAACTAAAGGAAGGTAAAACCATGCTGATACTTGGGGCACTGCCCCAACCTCATGG
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                                             CCCTCCAATCTCTCCATGTGGATGCTGCAGGAATCTCAG---ATGGTGGAACACTTGAGT
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Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analygis Group; Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Pujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Ishibiki, J., Kawamata, M., Yokomizo, S., Niikura, J., Kusunegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., Mirka, J., Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hayateu, M., Imorani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M. and Hayashizaki, Y.
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Intect Submission

Direct Submission

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Rujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,
Kodama, T., Kursoneki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J.,
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Sugiyama, A., Mareubara, K. and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,
Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,
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NIAS Rice Pull-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.

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hi, A. and Hayashizaki, Y.
Location/Qualifiers
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/ organism="Oryza sativa (j
mol type="mRNA"
/cultivat="Nipponbare"
/db xref="taxon:39947"
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HTG 30-NOV-2002

AP006053 122193 bp DNA linear HTG 30 Oryza sativa (japonica cultivar-group) chromosome 6 clone

RESULT 3
APO06053/c
LOCUS
DEFINITION

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Conscious bull and a constitute of a season of the screen control 
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Oryza satīva (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                                                                                                    Sasaki,T., Matsumoto,T. and Katayose,Y.
Oryza sativa nipponbare(GA3) genomic DNA,
clone:OSJNBb0026L12
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/mol_type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
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	GCCAAGGTAATCTGTTTTTGGGATGGGT 585	586 GGTTTAGGCAAGACAGCTCTTTCGAGGAAGAAGCGAAGAAGAAGAAGAAGAAGAAGAAGAAG	108585 SGIIISOGIAMANCIRIII COANGAMANIII GAARGAANAN AND CAANGAANAN	765 10846	766 CAAGGGAAGGTGGTAGTACATCATCTTTTCTGAGTACCTGATAGAAGAGCTCAAG	826 GAGAAGGGTACTITGITGITGIAGAIGAICIAIGGAITITACAIGAAITGGAAITGGAAITGGAAITGGAAITGGAAITGGAAITGGAAITGGAAITGGAAITGGAAITGGAAITGGAAITGIGGIA	886 AATGAAATTGCATTTCCTAAGAACAATAAGAAGGGCAGTCGAATAGTAATAACCACTCGG	946 AATGTTGATCTTGCGGAGAAGTGTGCCACAGCCTCACTGGTGTACCACCTTGATTTCTTG 108288 GATGTTGGCTTAGCTAAGGAGTGTACTTCTGAATTGCTTATCTACCAGCTTAAACCCTG	1006 CACATGAACGATGCCATAACATTGCTACTGAGAAAAACAAATAAAATTCATGAAGACATG 	1066 GAATCAAATAAAAATGATGAAAGATGGTTGAACGAATTGTAAATAAA	1126 CCATTAGCAATACTTACAATAGGAGCTGTGCTTGCAACTAAACAGGTGTCAGAATGGGAG 1185	1186 AAATTCTATGAACACTTCACAACTAGAAATAAACCCAAGCCTGGAAGCTTTGAGG 1245 108048 ACTTTTATGAACAAACAAACAAAAAAAAAAAAAAAAAAA	1246 AGAATGGTGACCCTAGGTTACAACCACCTACCATTGAAACCATGCTTTTGTAT 107988 AGGATACACCTTACAACTACTACCATCTATTTAGAACCATGCTTTTTGTAT 107988 AGGATACTCTTATATACTACTACTATCTATCTATCTTATAACTATTTTGTATTTTTATACTATCTTTTTAAACTATTTTTTATACTATCTTTTTATAACTATTTTTT	1306 CTAAGTATCTTTCCTGAGGATTTTGAAATCAAAGGAATCGTCTGGTAGGTA	1366 GCAGAAGGTTTGTTAGACCAAAGGTTGGGATGACGACTAAGGATGTCCGAGAAGTTAC	1426 ITTAATGAGCTAATGAGGGAGTATGATTGAGGGTGAGGGGGATAGGAGGA	1545		

ATTCTTAATCACTCAAAAA 1782 ||| || || || || || || || ATTTACTATCACAAAAT 107449 | |||| | | ACGCATTGCAAGATACAAT 107389 Trrcacaca----- 107218 CACACCTTTAGTTAGTCGC 2073 TCCTCCCTACTGAGGACA 2433 TGAGCAGCTCACTCACCTG 2493 ||||||||||||||||||| TGAGCGGCTCACTCACCTG 106744 CTTTAGTCTAAACCACCCA 2013 CAAAAGTTGCTGGTCTGAA 2133 TTACCTTGGGGAGAGCTA 2613 GATTTATGAATTGGATCAG 2673 ATTGGATTGGAGCATTATT 1662 ACATGCAGTTTGTCCAGAT 1722 AGACTTGCAGGTTCTAGAG 2193 GAGTATTGGA----- 1833 GGAAAAGATAGAAATAGGC 2733

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URL: http://cdnaol.dna.affrc.go.jp/cDNA/
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FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y.,
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Kishikawa-Hirozane,T. Kanagawa,S., Kanno,H., Kawai,J.,
Kishikawa-Hirozane,T., Natsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,H., Kouda,M.,
Sakazume,N., Salcoh,H., Sasaki,D., Sato,K., Shibata,K.,
Salcoh,H., Sano,H., Sasaki,D., Sato,K., Shibata,K.,
Tagami-Takeda,Y., Tagawa,A., Tagami,M.,
Tagawa,A., Tagawa,A., Takahashi,F., Toya,T., Waki,K.,
Tagami-Takeda,Y., Tagawa,A., Tagami,A., Toya,T., Waki,K.,
Tagami-Takeda,Y., Tagawa,A., Toya,T., Waki,K.,
Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M.,
Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K.,
Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J.,
Yokomizo, S. and Yoshimura, A.
Collection, mapping, and annotation of 28K full-length cDNA clones
from japonica rice
                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (31-JAN-2003) Shoshi Kikuchi, National Institute of
Submitted (31-JAN-2003) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (B-mailskikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 32K full-length cDNA clones from japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 GCCGGAGACGGTGGGGATGCCGATGTCGCTGCTGGGCAGCCCCTCGGGAAGGCCGC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110 CTCCGCCGCCGACGAGGCCACCTCCTGCTCGGCATCCAGAAGAGAGATCTGGTACAT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170 CAAGGACGAGCTGAAAACTATTCAGGCATTCTTAAGAGCTGCTGAAGTAACAAAGAAGAA 229
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Pred. No. 0;
0; Mismatches 858; Indels 15; Gaps
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/cultivar="Nipponbare"
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/clone="J023131G18"
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Best Local Similarity 70.77
Matches 2103; Conservative
                                                                                                                                                                                                                                                                                                                                          Kikuchi, S.
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AUTHORS
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106383 CACCCAAATTGTCCCGTGCTGCGAATGGCAATGGACCGAAGTGATCACGATCTTGCTGGC 106324
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FLI_CDNA; CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                2734 GAGTGCAGGTTGGAATCTGGGATTACTGGTATCATTCACCTTCCAAAGCTCAAGGAGATT
                                                                                                                                                                     106503 AGGTGCAGATTGGAATCAGGGATTATTGGTATCATTCACCTTCCAAGGCTCAAGGAGATT
                                                                                                                                                                                                                                                               2794 CCAATTAGATACGGAAGTAAAGTGGCTGGGCTTGGTCAGCTGGAGGGAAGTGAACGCA
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REFERENCE
AUTHORS
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Conservative 0; Mismatches
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Direct Submission
Submitted (23-AUG-2002) Madsen L.H., Department of Molecular
Submitted (23-AUG-2002) Madsen L.H., Department of Molecular
Biology, Aarhus University, Gustav Wieds Vej 10, DK-8000 C, DENMARK
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NBS-LRR disease resistance protein homologue; rga S-9202 gene.
Hordeum vulgare
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
2932 ATAGAAGTGCAAACAGCAGATCCTGTTCCTGATGCC 2967
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/organism="Hordeum vulgare"
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/cultivar="Regatta"
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URL: http://cdnaol.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length CDNA Froject Team: Kikuchi,S., Satch,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T.,
Yamamoto,M. and Nakahama,Y.,
FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y.,
Kobayashi,M., Kodama T., Kurcosaki,T., Kusumegi,T., Lu,M.,
Kobayashi,M., Kodama T., Kurcosaki,T., Tsunoda,Y., Ueda,M.,
Kie,O., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K.
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi,J., Alzawa,K.,
Akimura,T., Arakawa,T., Carninci,P., Pukuda,S., Hanagaki,T.,
Akimura,T., Arakawa,T., Carninci,P., Imotani,K., Ishiikawa Hirozane,T. Kanagawa,S., Kando,S., Kondo,M., Kagawa,T., Kanagawa,T., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N.,
Ota,Y., Saltoh,H., Sakai,T., Sagahe,Y., Tagami,M.,
Tagami-Takeda,Y., Tagawa,A., Takahashi,R.,
Tagami-Takeda,Y., Tagawa,A., Takahashi,R.,
Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K.,
Yasunishi,A., and Hayashizaki,Y.
                                                                                                                                                                           Direct Submission
Submitted (31-37N-2003) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
205-6602, Japan (E-mail:eKtuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007, Fax:81-22-838-7007, Fax:81-29-838-7007, Fax:
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/mol type="mRNA"
/cultivar="whipponbare"
/db raxe="taxon:3994"
/clone="Jol3103K24"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, P., Hotta, I., Iida, J., Ida, Y., Ikeda, R., Imamura, K., Imatari, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, M., Kawai, M., Kawai, M., Kodama, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Kodama, T., Kojima, K., Matsubara, C., Kurosaki, T., Kishimoto, N., Mixazaki, M., Matsubara, K., Matsuwama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Muraka, M., Nagata, T., Nakahama, Y., Nakamura, M., Namiki, T., Narikawa, R., Nilkura, J., Nishi, K., Ooka, H., Ooka, H., Osato, N., Otemo, Y., Ryu, R., Satoh, H., Sakai, K., Sakai, R., Sanishiki, T., Sagabe, Y., Shibata, K., Shinagawa, A., Shiraki, T., Saltoh, H., Sakai, K., Sugama, A., Shiraki, T., Shishiki, T., Sagabe, Y., Sugami-Takeda, Y., Tagawa, A., Takahashi, P., Takaku-Akahira, S., Tagami-Takeda, Y., Tagawa, A., Takahashi, P., Takaku-Akahira, S., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S., and Yoshimura, A., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S., and Yoshimura, A., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S., and Yoshimura, A., Suk, Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S.
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantes; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, BAC
clone.GSURBBO007020

L Published Only in Database (2001)

S Sasaki,T., Matsumoto,T. and Yamamoto,K.

Direct Submission

S Sasaki,T., Matsumoto,T. and Yamamoto,K.

Direct Submission

Submitted (04-APR-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8603, Japan

(E-mail:teasaki@abr.affrc.go.jp, URL;http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

The orientation of the sequence is from Ml3rev to -21Ml3 of the BAC
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chromosome 6,
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzae, Oryza.
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            AAGAAGATCTACTTATTGAGGAGCAAACTAAAGGAAGGTAAAACCATGCTGATACTTGGG
                                      GTGAAGATTCACTTATTCGGAAGCAAACTGAAGGAAGGTAAAACAGTACAGATACTCGGG
                                                               GCACTGCCCAACCTCATGGTCCTTCATCTTATCGGAATGCTTACCTTGGGGAGAAGCTA
                                                                                         GAACTGCCCAACCTCATGGTCCTGCAGCTTCGGTGGGGCGCTTATGTTGGGGGTGAAGCTA
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/mol type="genomic DNA"
/mol type="nipponbare"
/db xref="taxon:39947"
/chromosome="6"
/clone="OSJNBa0007020"
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Length 147363;

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Query Match

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                                                                       CTGGTATATCAAAGATGAGCTAAAAACGATGCAAGCATTCCTTAGAGCTGCTGAACTTAT
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2247 10650 2307 10590 2367 10470 2487 10413 2547	Db 10293 GAAGCTATTGTTCCGAGCAGAAGCATTCCCAAAACTC Qy 2667 GGATCAGCTAAGAGAGTTGAGATTTGAGCAGCAGC Db 10233 AGAGGACCTAAGAGAGTTGGAATTTGAGGCACCCC Qy 2727 AATAGGCGAGTTGGAATTTGAGTTACTGGT Qy 2787 GCAGATTCCAATTAGATACGGAATTATTGGG Qy 2787 GCAGATTCCAATTAGATACGGAAGTGATTGGGATGGATAGGA Qy 2787 GCAGATTCCACCCGTTGGAATCGGAATTATTGGG Qy 2787 GCAGATTCCACCCGTTGGAACTGGAATTATTGGGAAGGGAAGGGAAGGGAAGGGAAGGCAAGGGAAGGCAAGGCCCCGTTGGAACTGGAAGTGGCAAGGGAAGGAA	REFERENCE AUTHORS ACCESSION Oryza sativa (japonica cultivar-group) solution ACCESSION VERSION VERSION AP001168.1 GI:6983854 KEYWORDS Oryza sativa (japonica cultivar-group) Bukaryota; Vididiplantae; Streptophyta; Spermatophyta; Magnoliophyta; Liliopsid Enhartoideae; Oryzaa, Oryza AUTHORS JOURNAL AUTHORS AUTHORS Sasaki, T., Matsumoto, T. and Yamamoto, K. TITLE JOURNAL Direct Submission JOURNAL AGTObiological Resources, Rice Genome R
11787 TATCATCACAATTGGTGGACTTCTAGCTGCCAAAGATGTCAAAGAGTGGATTATA 11728 1194 TGAACACCTTCCTCAGAACTAGAAATAAACCCAGGAGTGTT 1168 11727 TGCACAAATTCCATCGGAACTTGAGAACACCCAAGCTTTGAAGTAATGAGGAGAGTGTT 1168 1154 GACCTTAGATTACAACCACCTTTGAAGCTTTGAAGTAATTGAGGAGTGTT 1168 11667 AGCCTTAGATTACAAACAACCCATCCATTTGAAACTAATTGAAGTAT 11608 11607 CTTTCCTGAGGATTTGAAAGGAACGTCTAGTGAGTTACTAAGGAT 11608 11607 CTTTCCCGAGGATTTGAAAGGAAACGTCTAGTGAGTTACTAAGGATGCAAAGGATTGCAAAGGAAACGTCTAGTGATTAGAATTGAAAAGGATTGAAAGAAA	1614 ATTCCATGGGGTATGATAAGAAACTGGTCGAGAAACATCCACATGTGGC 11308 1614 ATTCCATGGGGTATGATGATGATGGGATTGGGGCATTATTCGATGGC 1673 11307 CTTCTACATAGCAATAGCAACTGGATTGGATTGACGAAGTATAGC 1673 11307 CTTCTACATAGCAATAGCATGAGATTGACCAAGTCGGTCATTAAC 11248 1674 TATTTTGGTGAACACATAAAGAACTAACAATGACCAAGTCAGGTCATTAAC 11248 11247 AGTGTTTGGTGAAGAACTAACAACAACATTGTCCAAAAAGATTAAGGAT 11188 1134 GTTACGGGTCTTGGAATATTCAACAATTGTAATCACTCAAAAAGATTCGACG 1793 11187 GTTAAGAGTCTTGGAATTTTCAAGAGTTAGAATTGGAATGACAAAAAGATTCGACG 1793 11187 GTTAAGAGTCTTGAATTTTCAAGAGTTAGAATTTCGATGTAAAAAAATTTCCTAAA 11068 11127 TATATGGTCGGTGTCACTTGAAATATTCAAGATTCGGTGTGACTACAAAAAAAA	1887 ACAAACITTGAACATGCGGCCCTACCAAGTGAATCATAAACT 1946
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|||||||| | ATCTCTCCGCATAAATGCTTTTCGA 10531 TATTICATCTCCTCCCCTACT 2426 GCCTAACTGGATTGAGCAGCTCAC 2486 AAAGGAAGGTAAAACCATGCTGAT 2546 ||| |||| |||| |||||| |||||| |CTCGCCCAAATGGAAACAATAGA 10174 TATCATTCACCTTCCAAAGCTCAA 2786 GCTTGGTCAGCTGGAGGAGAAGT 2846 ATCTCTCCATGTGGATGCTGCAGG 2366 TAGAACACTTTGGATTTATGAATT 2666 CTCACCCCTGTTGGAAAAGATAGA 2726 GTCGACAAAGGAAAATGTAAGAT 2306 TTATCGGAATGCTTACCTTGGGGA 2606 CAGTGACCGAAGGTATCACGACCT 2906 linear PLN 21-MAR-2002 genomic DNA, chromosome 6, ı; Embryophyta; Tracheophyta; .da; Poales; Poaceae; , National Institute of Research Program; Kannondai NA, chromosome 6, PAC AGCAAATGAACC 9946 AACAGCAGATCC 2954

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.48378,48699. .48745,49124. .49342,
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/note="Similar to 22 kDa kafirin cluster; Ty3-Gypsy type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KQLHEALGTDIANFSTRYHPHTDGGTERVNQILEDMLAACALDFEGTWDRCLFYAFFSY
NNSYQASIKMSPNEAMFGRKCRTPLCWNEVGEALVFGPDILKSAEEGVKLIRERLKTA
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VAXQLELPEGLADVHNVFHVSQLKKCLRVPEEGVPLGNIELERNLTYKERPIKVLEST
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COMPIEMENT (32146. .35112)
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LEDKYDRLEKEIALLKKGEAPPQKARIRLTARKKRALFVPRYQLAPKYRVVEKEVAPAD
TPVIIISSDEGEESKRNHSKIEWVATQDDEDEPNEPSINLLCSEELE"
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PROPGSDRGSYLETEGIBNDATTKHLVBMLMAMDESRAETVLAAQDREDRNRGKICK
LEDKYDRLEKELAALKGEAPPQKARIRLTARKRALFYPRYQLAPKVRVVEKEVAPAQA
DPPVIIISSDEEEESKRNNSKIEWVATQDDEDEPSIDLRCLEELE"
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MKRDVABYVALCDICQRVKAEHQRPAGLLQPLPIPEWKWBBIGMDFITDLPRTPSGYD
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RQRRWLELIKDYDLGIHYHPGKANVVADALSHKAYCNIAQIRPDQDRLCRELEKLRLT
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PNKQKPRTPGQVGLRFCSSSYLWSDSSFPSSSSPISHRPIGGARSKRPPATMIYRNWS
                                                                                                                                                                                                                      join(28483. .28975,29105. .30435)
/note="Similar to 22 kDa kafirin cluster; Ty3-Gypsy type
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AU082144(E20182) correspond to a region of the predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(38728. .39519)
/note="Similar to gypsy-type retrotransposon RIRE8B DNA,
internal region (AB014741)"
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                                                                                                                                                              complement (25067. .28064)
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                                                                                                                                                                                                                                                                                                                                             /proteIn_id="BAA90794.1"
/db_xref="GI:6983859"
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/proteIn_id="BAA90795.1"
/db_xref="G1:6983860"
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/db_xref="GI:6983861"
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/protein_id="BAA90797.1"
/db_xref="G1:6983862"
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2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
The orientation of the sequence is from $P6 to T7 of the PAC clone. Genes were predicted from the integrated results of the following:GENSCANI.0, BLASTN2.0, BLASTN2.0 as well as $P91icePredictor (October1998 version). The genomic sequence was sparched against the non-redundant database NRP(PIR.SWISSPROT, GENPEPT, PDB) from MAFF DNAbank and the CDNA sequence database at RGP. Protein similarities of the cording regions were searched against NRP with BLASTN2.0. ESTS represent the identified CDNA sequences using BLASTN2.0 with the corresponding DDBJ accession no.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .16323,18384. .18477,19513. .20442))
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/db xref="G1:6983857"
/translation="MORSGRAKWAGRPKTAQARARGRGGERGPVDRAHHARSRGRGGT
RCTRAVRGGGGGGGTRSLTAGGTRAREGIDRGRLDPALAVLAPTWRLRGCHAGRRE
VDDDAGRNGRRSTAASDGANHGDTGKSEHTGRLHYTRGDEPTARIRRELEGGSSRRR
OPAAGEEENGDEVARGQPPAARASTRLRESDASVGLGGTTPSEAGDERRFRARAATAA
                                                                                                                                                                                                                                                                                                                                                                                              Detailed information on assemble quality together with annotation of this entry at http://www.dna.affrc.go.jp:82/genomicdata/GenomeFinished.html.
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GRLRPRRRVAEIHQQVCALVASNPSSRRRCSLSTCRRRDSIDMSSFCTIGIFLIDQGI
SQHAGRQQRRDPSASWAAIRSMSTAILRAAHRQSRRRRPIHQQKAVLETSQHPLTASA
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LGPKWAAMSVWERGTDIGRSRRELALGACGQNGGGGRMTPAGRCKEKEGEKRGLAPLP
LWGKGGGGGATRQREGGLCLRPLEASARSGGAEAMTTAMTAGRFGAKIJAAATGRSAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MAELPPNDDAIVMQDKEEEVEEKIVEEEKPSAPAAEVNNTEVVE
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Grgsrarargaraerkgeregesgsapgerarererkrapgregemgregfgpsnpg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="EST AU082143(E4368) corresponds to a region of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="Similar to 22 kDa kafirin cluster; Ty3-Gypsy type
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/note="Similar to gypsy-type retrotransposon RIRE8B DNA,
internal region (AB014741)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(2859. .3254,3286. .3498,3504. .3752,3923. .4483,4546. .4662))
/note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (japonica cultivar-group) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(1092. .1123,1482. .1740,1821. .2060)
note="hypothetical protein"
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/db_xref="GI:6983855"
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/db_xref="G1:6983856"
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/organism="Oryza sativa
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/db_xref="GI:6983858"
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/cultivar="Nipponbare"
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/chromosome="6"
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TGATCTTGCGGAGAAGTGTGCCACAGCCTCACTGGTGTACCACCTTGATTTCTTGCAGAT 1010
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                                                                                             TATGATACGCCAACTTCTTGGCCCCCAGTTCTCTGGATCAACTCTTGCAAGAATTGCAAGG
                                                                                                                                                                       GAAGGTGGTGCAAGTACATCATCTTTCTGAGTACCTGATAGAAGAGCTCAAGGAGAA
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                     CCCTTGCAATGCTTGGATTACAGTGTCACAATCATTTCACAGGATTGAGCTACTTAAAGA
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                                                                      / POCOLETIA 164 = BAA90799.1"

/ protein id= "BAA90799.1"

/ db xref="G1:6983863"

/ db xref="G1:6983863"

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KLVGEPOTPKKELLDKINMDANDDHCRVLCVWGMGGAGKTTLVWRTREBKENIDEA
KLVGEPOTPKKELLDKINMDANDDHCRVLCVWGMGGAGKTTLVRKTEREKERIEVY
RADIMNTDHWEWIREFALPSKNNKRSRVIVTTRLDGVANACTTEPFVYRLKLLETEC
AIDLLARWGESKEDMKNDNNLKSIYTQLFSHLKFCYLYLSIFPEDIEIRRRHLVNR
WYAGGLVRARVGMTISDVGESYFDELISRSMAGPRRYSSSRWEEM
CROLPSELENNPSPGVAAIRRVVTLSYGHLPSHLKFCYLYLSIFPEDIEIRRRHLVNR
WYAGGLVRARVGMTISDVGESYFDELISRSMAGPRSRVMEGHWGSCRYHDIMRDIIVS
ISKEENFYYSTGDNVSTVIVEKFRHLSCHGGNYPIVGNDFSRYRKLIVFREEPOTP
VGSSIGAOFTMLRVLDLENNYFSYTGNINKTGLLRHLRYLMTRRRSTIYALDSS
IGKLQNLQYLDIRESBEISTLEPTDISKLLMERILNFRRETIYALDES
IGKLQNLQYLDIRESBEISTLEPTDISKLLMERILNFRRETIYALDES
IGKLQNLQYLDIRESBEISTLEPTDISKLLMERILNFRRETIYALDES
IGKLQNLQYLDIRESBEISTLEPTDISKLLMERILNFRRETIYALDES
IGRUNTTPLVGSAARNYTIAELHRAYSSHWSETFOVENYFOTSONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(59365. .59367,59518. .59647,61034. .61132,61435. .61862,
31902. .62036)
note="hypothetical protein"
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TLEWLGPCNFSPPPLLRKLELHGRIRVMPDSFRNLKQLRKI FLRLSELDGRAI EILGT
LPNLMLLNLDGRAYVGNELAFKKHEFPNLKELRI SMLSELRGIRFEKDALPHMERMEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MKSWKFVCRKVLIDGKVGSLKKNFCTKLGONELDODINDLNICA
DFLPIKGKIESETDLITARSTVSTNTYDLKKGYPWASPANSCSPAGELLLPHTGELLH
ARRRAPPPPCLRAPDAHAGSGTWRTSAARPTGRSIHAANDGGPRATAALTRGGCRGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATTGAAGATTCCCTTGATGAATTTAAGGTCCATATTGAAAGCCAAACCCTATTTCGTCA
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LLSSTVVIMGGVATAGLAGIFLFGGKEKFQNYLCREGERLRQQDRAAMGKN"
complement(join(54820. .57727,58608. .58723))
/note="Similar to gene for Pib (AB013448)"
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Pred. No. 1.1e-280;
0; Mismatches 936; Indels
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/protein_id="BAA90799.1"
/db_xref="GI:6983864"
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Best Local Similarity
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1716 TCCAGATCAATTGAGGATGTTACGGGTCTTGAAGATGTGACATTCTTAATCAC 1715	AACTITGAACATGCCGAGCACATACATTGCAGCACTACCAAGTGAGATCAGTAAACAGTGAACACATAACAAGTGAACACATAAGAACACATTGCAAATTTCTACACTACCAACTGATATCGTAAGCAAGTGTAACACTTTTTTTT	GGTTCTAGAGTATGTAGATATCAGGGGACCAGTAGTAGAGCAATCAAAGAGCTGGGGCA	55291 AGAGATACTIGGAACACTACCCAACCTCGTGAATCTCGATGGCAGAGCATATGT 55232 2601 TGGGGAGAACCTACCCAACCTCCTGAATCTCGATGGCAGAGCATTTA 2660 [

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                                                                                                            GCTTGGGTCACTGTGTCACAGTCATTTGTCAGACAGAGAGCTCCTGAGAGCTAATCAAG
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                                                                              GCTGAGCTTGTTGGGTTTTCTGACTCCAAGAAAAGGCTGCTTGAAATGATCGATACCAAT
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L. 4248
/organism="Oryza sativa (japonica cultivar-group)'
/mol_type="mRNA"
/cultivar="Nipponbare"
/db.xref="taxon:39947"
/clone="J023064A19"
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Laboratory of Gene Expression; 2-1-2 Kannondai, Tsuku
305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28K full-length cDNA clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 811.6; DB 8;
Pred. No. 1.1e-203;
0; Mismatches 1074;
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2632 TTCCCAAATCTTAGAACACTTTGGATTTATGAATTGGA 3179 TTCCGAGGGCTCAAAGACTCTTCGACTTGAACTCTTTGGA 2692 GAGGACGCAGCTCACCCTGTTGGAAAGATAGAAATA 2692 GAGGAGGAGCTCACCCTGTTGGAAAGATAGAAATA 2752 GGGATTACTGGTATCATTCACCTTCCAAAGCTCAAGGAC 2752 GGGATTACTGGTATCATTCACCTTCCAAAGCTCAAGGAC 2752 GGGATTACTGGTATCATTCACCTTCCAAAGCTCGAGAA 2812 AAAGTGGTGGGCACGGTCAGCTGGAGAGGAAGTGAAC 2812 AAAGTGGTGGGCTTGGTCAGCTGGAGAGGAGAAGTGAAC 3359 AAACTGGTGAAGCGTCCTGGTGAAGCTCGAGAAG	RESULT 10 AK071029 LOCUS DEFINITION OTYZA GALIVA (japonica cultivar-group) cf insert sequence. ACCESSION AK071029 VERSION AK071029 VERSION AK071029 OTYZA GALIVA; CAP LTAPPET. OTYZA GALIVA; CAP LTAPPET. OTYZA GALIVA (japonica cultivar-group) ORGANISM OTYZA GALIVA (japonica cultivar-group) ORGANISM OTYZA GALIVA (japonica cultivar-group) ELARIVORS OTYZA GALIVA (japonica cultivar-group) ELARIVORS ELARIVORS AGRACIO (japonica cultivar-group) OTYZA GALIVA (japonica cultivar-group) ELARIVORS ELARIVORS AGRACIO (japonica cultivar-group) OTYZA GALIVA (japonica cultivar-group) ELARIVORS ELARIVORS AGRACIO (japonica cultivar-group) OTYZA GALIVA (japonica cultivar-gro	Ohtenki, K., Shishiki, T., Foundation of Ac Jean-Cenec Genome Sequencing & Analysis Grolids. T., Sugano, S., Fujimura, T., Suzuki,) Kurosaki, T., Kodama, T., Masuda, H., Kobaye Narikawa, R., Sugajama, A., Mizuno, K., Yokk Ikeda, R., Tshibiki, J., Kawamata, M., Yoshi Kawai, J., Carninoi, P., Adachi, J., Aizawa, Hara, A., Hashidume, W., Hayesu, N., Imotar, Kagawa, I., Kondo, S., Konno, H., Miyazaki, P., Salto, R., Sasaki, D., Sato, K., Shibata, K., Yoshino, M. and Hayashizaki, Y., Shibata, K., Yoshino, M. and Hayashizaki, Y., Shibata, K., Yoshino, M. and Hayashizaki, Y., Hayasaki, P., Solence 301 (5631), 376-379 (2003) MEDLINE Science 301 (5631), 376-379 (2003) REFERENCE 2 (bases 1 to 2015) Adachi, J., Aizawa, K., Akimura, T., Hayashizaki, Y., Hayashida, K., Hayashizaki, Y., Hayasta, I.K., Hori, F., Hotta, I., Ilda, J., Iida, Y., Ishika Hori, P., Hotta, I., Ishika, Kanagawa, S., Katchi, Hayashida, Y., Matashira, N., Kanagawa, S., Kurihara, C., Kurosaki, T., Kusume Masuda, H., Matsubara, K., Matsuyama, T., Mishi Mizuno, K., Murakami, K., Muraka, J., Nishi Numasaki, T., Narikawa, R., Nikura, J., Nishi Numasaki, T., Narikawa, C., Chomo, Y., Ryu, R., Saltco, M., Ota, Y., Otomo, Y., Ryu, R., Saltco, M., Ota, Y., Otomo, Y., Ryungaya, M., Ota, Y., Otomo, Y., Ryungaya, Y., Narikawa, Y., Narikawa, Y., Narikawa, Y., Narikawa, Y., Narikawa, M., Ota, Y., Otomo, Y., Ryungaya, Y., Nangaya, Y., Nang	Sakazume, N., Sano, H., Saeaki, D., Sato, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami Tagawa, A., Takahashi, F., Takaku-Akahira,
1558 TTATTACCAATGGGTGATATCGCAATTTCTATTTCCGCAGAGAATTTCGTA 2148 1558 TTATTACCAATGGGAGATGGCTCTGATTTAGTTCGGAAACACTCGCCACATAGCATTC 1617 1619 TTCATGACGAAAGGGTTTGTTTCGATTTGAAAACATCCATC		2092 ATTGCTGAATTGCACATGGCCACCAAAGTTGCTGGATCAATCGTGTGAAGGTA 2151 2686 GTGGCGAGTTCCGCAAGG	
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ra,S., Tanaka,T., Tomaru,A., ATCAGCTAAGAGATTT 2691 TAGGCGAGTGCAGGTTGGAATCT 2751 AGATTCCAATTAGATACGGAAGT 2811 AAATTAAGTATTTTGCAAAAGGG 3358 GCCAAAGTGCGCATCATCGGGAG 3418 linear PLN 24-JUL-2003 cDNA clone:J023075E16, full ACGCACACCCAAATCGCCCGTG 2871 over 28,000 cDNA clones from Embryophyta; Tracheophyta; la; Poales; Poaceae;

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                                                                                                                                                                                                                                                      and
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Tel.129-838-7007, Pas. 812-29-838-7007,
This clone is one of the 28K full-length cDNA clones from japonica
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URL: http://cdnaol.dna.affrc.go.jp/cDNA/
URL: http://cdnaol.dna.affrc.go.jp/cDNA/
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Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T.
Yamamoto,M.
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Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S.
Yoshimura,A.

    2015
/organism="Oryza sativa (japonica cultivar-group)"
/orltivar="Nipponbare"
/db xref="Laxon:39947"
/clone="J023075E16"

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The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi, S., Satch,K., Nagatea,T., Kawagashiza,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Oboka,H., Hotta,I., Kojima,K., Namiki,T., Chneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T., Foundarion of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo,Y., Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Murakami,K., Inda,Y., Rusuma,A., Mazuho,K., Yokomizo,S., Niikura,J., Ikeda,R., Ishibiki,J., Kawamata,M., Yokomizo,S., Niikura,J., Ikeda,R., Ishibiki,J., Kawamata,M., Yokomizo,S., Niikura,J., Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN:, Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hasyatuwa,M., Mayatsu,N., Imotali,Y., Ishii,Y., Itoh,M., Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y., Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
                                                                                                                                                                                                                                                                                                                   997 GATITCITGCAGATGAACGATGCCATAACATTGCTACTGAGAAAAAACAAATAAAAATCAT 1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AALU1823 GIVA (japonica cultivar-group) cDNA clone:J033067K01, full insert sequence.
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                                                                                                                                                                                                                                                           358 ACAACACGAGATGTGGCTTGGCTGCGAAGTGCACTTCAGATTCACTCATCTACCACCTC 417
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
                                238 AAGCTAGAGGACATGAGATACTTTATTGTTCTTGATGACTTGTGGACCATAGATGCTTGG
                                                                                                                            298 GATTGGATCAAATCTATTGCTTTTCCTATTAGAAACAATAAAGAAGAGCCGAATATTAATA
                                                                                                                                                                                                                                                                                                                                                                           478 gaagacangaaaanganaagaaanganggcagnggcaaaaanggnaagaagngn
                                                                                        877 AATTGGATAAATGAAATTGCATTTCCTAAGAACAATAAGAAGGGCAGTCGAATAGTAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                   1057 GAAGACATGGAATCAAATAAAAATATGCAAAAGATGGTTGAACGAATTGTAAATAATGT
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Direct Submission
Submitted (122-AUG-2002) Madsen L.H., Department of Molecular
Submitted (122-AUG-2002) Madsen L.H., Department of Molecular
Biology, Aarhus University, Gustav Wieds Vej 10, DK-8000 C, DENMARK
                                                                                                                                                                                       HVU506137 564 bp DNA linear PLN 28-APR-2003
Hordeum vulgare partial rga S-9202 gene for NBS-LRR disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /trānslation="GMGGVGKTTLARKVYESKEDIVNKFACCAWITVSQSFSKIEMLK
BMIQLIGFELLRQCLKELEBEKAVHVEDLASYLREKLEDMRYFIVLDDLWTIDAWDWI
KSIAFPIRNKDSRILITTRDVGLAKCTSDSLIYHLKHLQIEDATNLLLRKSRKTWE
DMKNDKRYMAVVNKOYRKCGGLPFALIT"
                                                                                                                                                                                                                                                                                                                                        NBS-LRR disease resistance protein homologue; rga S-9202 gene. Hordeum vulgare
Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'product="NBS-LRR disease resistance protein homologue"
'protein_id="CAD44593.1"
'db_xref="GI:28555850"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Madsen, L.H., Collins, N.C., Rakwalska, M., Backes, G., Sandal, N., Krussell, L., Jensen, J., Waterman, E.H., Jahoor, A., Pryor, A.J., Langridge, P., Schulze-Lefert, P. and Stougaard, J. Barley disease resistance gene analogs of the NBS-LRR class: identification and mapping Mol. Genet. Genomics 269 (1), 150-161 (2003)
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    564
    /organism="Hordeum vulgare"
/mol_type="genomic DNA"
    /cultivar="Regatta"

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1438 ATCAACCGAAGTATGATTCAAC 1459
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1993 ATCAATAGAAGCATGATTCAAC 2014
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codon_start=1
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                            2014 GGCTAATCTATTTTTTGCCAAACTATGCTGTCGCCATCGAATCGCCATGCAGCTACAA
                                                                                                                                                                                                                                                                                                                                                                                                                     CCTATITICC------TCTGGCACAGAGATIGACAIGGATICCTAIGCAGAAGAC
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                                                                                                                                                                                                                                                                               AACCTTAAATCAAGAGTTGAAGAAGTGAGTAGCAGGAACACACGCTACAGTTTAGTCAAG
                                                                                                                                                                                                                                                                                                                                                2074 GAGCTAAAGGCCCGTGCACAGGATGTCAGTGAGCGGCGTTCACGCTATGAGGTGATGCTG
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Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T., Haraoka,T., Haraoka,T., Iida,J., Imamura,K., Imotani,K., Ishii,Y., Itch,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J., Kohia,X., Katoh,H., Kawai,J., Kohia,X., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Kishikawa-Hirozane,T., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Nimasaki,R., Ohno,M., Osato,N., Sasaki,D., Sato,K., Shibata,K., Shibata,K., Shibata,K., Shinagawa,A., Shiraki,T., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Tayawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K., Yasunishi,A. and Hayashizaki,Y.
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Numasaki,R., Ohneda,E., Ohno,M., Ohtsuki,K., Oka,M., Ooka,H., Osato,N., Ota,Y., Otomo,Y., Ryu,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato, K., Satoh, K., Shibata,K., Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S., Shinagawa,A., Suzuki,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,Y., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Tsunoda,Y., Veda,M., Waki,K., Xie,Q., Yahagi,W., Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and
                                                                                                                                                                                                                                                                                                                                                                             Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nasa.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
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URL: http://cdnaol.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi.S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. Yamamoto,M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, W., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ooneda, E., Yahagi, W., Suzuki, K., Li, C., Ohseuki, K., Shiliki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Teunoda, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Woshyashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mazuno, K., Vokomizo, S., Niikura, J., Kadawa, T., Koka, M., Kauno, H., Matsubara, K., Rikkni, Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayateu, N., Imotani, K., Ishii, Y., Itoh, M., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M. and Hayashizaki, Y., Yoshino, mapping, and annotation of over 28,000 cDNA clones from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, N., Hiramoto, K., Hiraoka, T., Hayashizaki, Y., Hayastau, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, Y., Ieda, R., Imanura, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kivuchi, S., Kishikawa-Hirozame, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, R., Niikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa (japonica cultivar-group) cDNA clone:J033048003, full AK073612
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3022 CAAGTGTTAACCCTGAGCTATAATGATCTACCTTACCATCTGAAGGCCTGCTTCTTGTAT 3081
                                                            CTAAGTATTTTTCCTGAAAATTATGTGATCAGGAGGGGCCTTTGGTGAGGAGGTGGGTA 3141
                                                                                                                                                                                    GCAGAAGGGTTTGTTAGACCAAAGGTTGGGATGACGACTAAGGATGTCGGAGAAGTTAC 1425
                                                                                                                                                                                                                                                                                                      TTTAATGAGCTAATCAACCGAAGTATGATTCAACGATCAAGAGTGGGCATAGCAGAAAA 1485
                                                                                                                                                                                                                                                                                                                                                                                                                              1486 ATTAAGACTIGICGAATTCATGATATCATCGIGATATCACAGTTTCAATCTCGAGACAG 1545
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FLI_CDNA; CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;.
Enrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                  3142 GCCGAAGGTTTTGTCAACCAAAGGCATGGACTAAGCATGGAAGATGCCGAAAGTTAC
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Science 301 (5631), 376-379 (2003)
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FAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., FAIS Genome Sequencing & Analysis Group: Otomo, Y., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kursumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Sugiyama, A., Matsubara, K. and Murakami, K. Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hiraoka, T., Hanagaki, T., Hiraoka, T., Hori, F., Iida, J., Immura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katch, H., Kawal, J., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakai, C., Sakai, K., Sakazume, N., Sano, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shinagawa, A., Tayakashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A., and Hayashi, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      URL: http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
                                                                                                                                                                                                                                                                                                                                                                         Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail-skikuchi@niss.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007, Table one of the 28K full-length cDNA clones from japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                814
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Osato, N., Ota, Y., Otomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakai, M., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, Shiangawa, A., Shitaki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takhashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Yoya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, O., Yahagi, W., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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49.6%; Pred. No. 1.6e-43;
vative 0; Mismatches 756;
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/cultivar="Nipponbare"
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/clone="J033048003"
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es 832; Conservative
                                                                                                                                                                                                                                                                                                                                                Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                            AAGGTGAGGAGCTGCATGATTTGATGTTAGATGTCATTGTCTCCAGGTCAATT 2362
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Jayasaaka, H., Katayose, Y. and Sasaki, T.
The Pib gene for rice blast resistance belongs to the mucleotide
binding and leucine-rich repeat class of plant disease resistance
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                                                              TATCTAAGTATTTTCCCTGAAAATTATGTGATCAAGAGGGGACCCTTGGTGAGAAGGTGG
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/tissue type="green leaf"
/clone lib="cDNA leaves inoculated with Pyricularia
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/mol_type="mRWA"
ferrain="Tohoku IL-9"
/db_xref="taxon:4530"
/chromosome="2"
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46.6%; Pred. No. 9.1e-41;
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Matches 1002; Conservative 560 1429 1489 1549 733 848 806 1906 1609 793 1729 1028 1088 1966

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1262	STIACAACCACTACCATTIGAAACCATGCTTITIGIATCTAAGTATCTTTCCTG 1321
1322	PAGGATTTTGAAATCGAAAGGAATCGTCTAGTAGGTAGGATAGCAGAAGGGTTTGTTA 1381
1382	9 GACCAAAGGTIGGGAIGACGACTAAGGAIGICGGAGAAAGTIACTITAAIGAGCIAATCA 1441
1442	9 accgaagtatgattgaacgatcaagagtgggcatagcagaaaaattaagacttgtcgaa 1501
1502	PITCAIGAIATCAICCGIGAIAICACAGITICAAICTCGAGACAGGAAAAITTIGIATIAI 1561
1562 2446	PACCAATGGGAGATGGCTCTGATTTAGTTCAGGAAAACACTCGCCACATAGCATTCCATG 1621
1622	9 GGAGTATGTCCTGCAAAACTGGATTGGAGCATTATTTGTTGTTGTGTGTTTTTTG 1681
1682	grgacagacccaagagtctagcacatgcagttrgtccagatcaattgaggatgttaggg 1741
1742	TCTTGGATCTTGAAGATGTGACATTCTTAATCACTCAAAAGATTTCGACGTATTGCAT 1801
1802	TGTTGTGCCACTTGAATACTTGAGTATTGGATATTCGTCATATATTCACTTCCCA 1861
1862	GATCCATTGGTAAACTACAGGCCTACAAACTTTGAACATGCCGAGCACATACAT
1922	
1982	: TTCATTATGACAACTTTAGTCTAAACCACCCAATGAAGTGCATAACTAAC
2042	
2102	: TGCACATGGCCACCAAAAGTTGCTGGTCTGATCAGTGTGTGAGGGTACCCAAAGGAA 2161
3022	TAGGTAAGTTGCGAGACTTGCAGGTTCTAGAGTATGTAGATATCAGGCGGACCAGTAGTA 2221
2222	: GAGCAATCAAAGAGCTGGGGCAGTTAAGCAAGCTGAGGAAATTAGGTGTGACAACAAACG 2281

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FAIG Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., Ramamata, M., Kobayashi, M., Kodama, T., Kursumegi, T., Lu, M., Masuda, H., Miura, J., Kodama, T., Kursumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Nikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Sugiyama, A., Matsubara, K. and Murakami, K. Genome Exploration Research Group in Riken Genomic Science Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hayalida, K., Hayatsu, N., Hizamoto, K., Hiramoto, K., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Kach, H., Kawai, J., Kondo, S., Konno, H., Konda, M., Kojawa, I., Kojima, Y., Kondo, S., Konno, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sakai, C., Sakai, K., Sakazume, N., Tagami, M., Tagami, M., Tagami, M., Tagami, M., Tagami, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A., and Hayashizaki, Y.
                  Kanagawa, S., Katoh, H., Kawagashira, J., Janikawa, T., Loui, T., Kawanata, M., Kikuchi, S., Katoh, H., Kawagashira, N., Kawani, J., Kawanata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kodima, Y., Kondo, S., Konno, H., Kouda, M., Kodama, T., Kojima, Y., Kodima, T., Musuka, J., Miura, J., Lui, C., Lu, M., Masuda, H., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, R., Nikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohteuki, K., Oka, M., Ooka, H., Sakazuno, N., Ota, Y., Otomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Shibaika, T., Salo, H., Sasaki, D., Satoh, K., Shibata, K., Shibaika, T., Shibaika, T., Sogabe, Y., Sugano, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Yamamoto, M., Waki, K., Xie, O., Yahagi, W., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           URL: http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
    ., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 1059-6802, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax.81-29-838-7007, Pax.81-29-88K full-length cDNA clones from japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        680 AATCATTTCACAGGATTGAGCTACTTAAAGATATGATAC-----GCCAACTTCTTGGC 732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90 ;
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Oryza sativa (japonica cultivar-group) cDNA clone:J013043101, full
insert sequence.
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                                               CCTTGCTCAAAAACCTCAAAAAGCTAACCCAACTGTGTAAACTAGGTGTGAC-----TG 3132
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FLI_CDNA; CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Bhrhartoideae; Oryzeae; Oryza.
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japonica rice
Science 301 (5631), 376-379 (2003)
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The invention relates to novel broad-spectrum resistance gene Fiz and Luc NBS(1-6) genes present in the Pi2 gene cluster region. The rice Pi2-like disease resistance nucleic acid molecules are useful for enhancing disease resistance in plants. The present sequence represents a cDNA encoding a rice NBS4 polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 2951.6;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; SEQ ID NO 13; 120pp; English.
ВЪ
                                                                                                                                 O. minuta Pi2 region contiguous
ADM72250 standard; DNA; 99090
                                                                                                                                                                                                                                                                                                                                                                                                                               09-SEP-2002; 2002US-0409216P.
18-MAR-2003; 2003US-0455713P.
05-SEP-2003; 2003US-00656394.
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Best Local Similarity 99.9°
Matches 2954; Conservative
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                                                                                                                                                                                                                                                  Oryza minuta.
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1515	80093 TTCATCTTATCGGAATGCTTACCTTGGGGAGAAGCTAGTATTCAAAACAGGAGCTTCC 80152
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Length 3096;

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blight and rice blast resistance genes). The DNA sequences may be used a markers for resistance to infection with Magnaporthe grisea in plant breeding programs. The present DNA sequence represents an NBS gene from the Oryza minuta Pl9 locus.
                                                                                                                                                                                                                                                                                                                                                        121 ATCAAAGATGAGCTAAAAACAATGCAGGCATTCCTTAGAGGCTGCTGAAGTTATGAAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                         GATTCCCTTGATGAATTTAAAGTCCATATTGAAAGCCAAACCCTATTTCGTCAGTTGGTG
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                                                                                      C; 730 G; 800 T; 0 U; 0 Other;
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                                                                                                                       DB 12;
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                                                                                                                     Query Match 94.1%; Score 2916.2; Best Local Similarity 96.8%; Pred. No. 0; Matches 2975; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2 and NBS3, useful for producing plants resistant to Magnaporthe grisea
                                                                                                                                                                                                                                                                                                   TAATGTACAGTGACCGAAGGTATCACGACCTGGGGCTGAAGCCCGAAGGATCTTCTATAG
                                                                                                                                                                                                                                                                                                                                                                      CAACGGATCCCCTTCCCGAGCAGCAGGAGAGAGAGCTCGCAGTCGCAGTCGAGCTGATCACGTTGA
 CAAATCTTAGAACACTTTGGATTTATGAATTGGATCAGCTAAGAGAGATCAGATTTGAGG
                   ACGGCAGCTCACCCCTGTTGGAAAAGATAGAGAATAGGCGAGTGCAGGTTGGAATCTGGGA
                                                                                          TTACTGGTATCATTCACCTTCCAAAGCTCAAGGAGATTCCAATTAGATACGGAAGTAAAG
                                                                                                                                                        TGGCTGGGCTTGGTCAGCTGGAGGAGAGTGAACGCACCCAAATCGCCCCGTGCTGC
                                                                                                                                                                                                                              TAATGTACAGTGACCGAAGGTATCACGACCTGGGGGCTGAAGCCGAAGGATCTTCTATAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          binding site; NBS; Pi9 gene; bacterial blight; rice blast; ling; transgenic plant; plant; gene; ds.
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01-FEB-2002; 2002US-0353304P.
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P-PSDB; ADIS7172.
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10   CCTARGANCATTARGARGGGCACTCCACTGATTTCTTCCACATGATCTCTCCC   102   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104   104	

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                                                                                                                                       GAAGTGAGTAGCAGGAACACACTACAATTTAGTCGAGCCTATTTCCTCCGGCACAGAG
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                                                                                              GTCTTGGATCTTGAAGATGTGACATTCTTAATCACTCAAAAAGATTTCGACCGTATTGCA 1800
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                                                       AACCGAAGTATGATTCAACGATCAAGAGTGGGCATAGCAGGAAAAATTAAGACTTGTCGA 1500
                                                                  GGTGACAGACCCAAGAGTCTAGCACATGCAGTTTGTCCAGATCAATTGAGGATGTTACGG 1740
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GAGGATTTTGAAATACAAAGGAATCGTCTAGTAGGTAGATGGATAGCAGAAGGGTTTGTT 1380
                 TCTATTTCATCTCCTCCTCCCCTACTGAGGACACTCGTGTTGGATTGTTGAGGAG
                                                                                                                                   TTACCAATGGGAGATGGCTCTGATTTAGTTCAGGAAAACACTCGCCACATAGCATTCCAT
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The invention comprises binding site (NBS) prott blight and rice blast remarkers for resistance to breeding programs. The lot oryza minuta Pi9 loc
                                           Nucleic acids encoding
and NBS1, useful for pi
infection.
                                                                               Claim 3; SEQ ID NO 92;
                                                                                                                                                              Sequence 3276 BP; 1026
                WPI; 2004-121064/12.
P-PSDB; ADI57176.
Liu G;
Wang G,
#X##X###X#X#X
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Query Match Best Local Similarity 9 Matches 2900; Conservati CAATGCTAATGAT 294 GTATATCAAAGAT GGTGAAACTCAGA TGAAGAAGTGAGT 594 AGAGATTGACATG CAATGCTAATGAT GACAGCTCTTTCG ACGCCAACTICTA 117 GTATATCAAAGAJ AAAGAAAGATGAA NAAGAAAGATGAA GGTGAAACTCAG TGAAGAAGTGAGT AGAGATTGACATC TGAAGCTGAGCTT GACAGCTCTTTCC CAATGCTTGGATT CAATGCTTGGATT ACGCCAACTTCTT 837 CTTTGTTGTTCTP TGAAGATTCCCT TGAAGATTCCCT TGAGGCTGAGCT GGTGGTGCAAGT 597 474 537 177 354 414 357 417 654 657 237 297 534 477 714 774 834 717 894 777 g ò g ð g ઠે 8 6 8 Q ઠે g 8 8 8 g ઠે g ઠે ద ઠે 중 음 ò

	   Db 1014 CTTT	
	Qy 897 ATTT	897 ATTICCTAAGAACAATAAGAAGGGCAGTCGAATAGTAATAACCACTCGGAATGTTGATCT 956
ng nucleotide binding site (NBS) proteins NBS1, NBS2 producing plants resistant to Magnaporthe grisea	Db 1074 ATT	cctaagaacaataagaaggggggggtggaatagtaataaccactcggaatgttgatct 1133
2; 136pp; English.	Qy 957 TGCG       Db 1134 AGCG	TGCGGAGAAGTGTGCCACAGCCTCACTGGTGTACCACCTTGATTTCTTGCAGATGAACGA 1016
ses the amino acid and coding sequences of nucleotide	1017	
roteins from the Oryza minuta Pi9 locus (bacterial t resistance genes). The DNA sequences may be used as	1194	
ce to intection with Magnaportne grisea in plant he present DNA sequence represents an NBS gene from locus.	Oy 1077 AAAT	AAATATGCAAAAGATGGTTGAACGAATTGTAAATAAATGTGGTCGTCTACCATTAGCAAT 1136
28 A; 631 C; 770 G; 847 T; 0 U; 0 Other;	1254	
%; Score 2850.2; DB 12; Length 3276; 2%; Pred. No. 0;	Oy 1137 ACTT.      Db 1314 ACTT.	ACTIACAATAGGAGCTGTGCTTGCAACTAAACAGGTGTCAGAATGGGAGAAATTCTATGA 1196 
LIVE U; MISHBACCHEB 83; INDEIB U; GADE U; ATGAGCTAAAAAACGATGCAAGCATTCCTTAGAGCTGCTGAACTTATGAA 176	Oy 1197 ACAC       Dh 1374 ACAG	ACACCTTCCTTCAGAACTAGAAATAAACCCAAGCCTGGAAGCTTTGAGGAGAATGGTGAC 1256
atgagctaaaaacgatgcaagcattccttagagctgctgaacttatgaa 353 aactattaaaggtttgggcagagcaaatacgtgacctgtcatatgacat 236	1257	
TTGATGAATTTAAGGTCCATATTGAAAGCCAAACCCTATTTCGTCAGTT 296	Oy 1317 TCCT           Db 1494 TCCT	TCCTGAGGATTTTGAAATCAAAAGGAATCGTCTAGTAGGTAG
	Oy 1377 TGTT      Db 1554 TGTT	TGTTAGACCAAAGGTTGGGATGACGACTAAGGATGTCGGAGAAAGTTACTTTAATGAGCT 1436 
GAGAACGCCACCGAATIGCTAICCGTAICCACAACCTTAAATCAAGAGT 533 GTAGCAGGAACACGCTACAGTTIAGTCAAGCCTATTTCCTCTGGCAC 416	Qy 1437 AATC      Db 1614 AATC	1437 AATCAACCGAAGTATGATTCAACGATCAAGAGTGGGCATAGCAGGAAAAATTAAGACTTG 1496 
stagcaggaacacacgctacagtttagtcaagcctatttcctctggcac 593 rgcattcctatgcagaagacattcgtaatcagtcagctcgcaatgtgga 476		
	Db 1674 TCGA Ov 1557 ATTA	tcgaatccatgatatcatccgtgatatcacagtttcaatctcgagacaggaaaattttgt 1733 attattaccaatgggagatggctctgatttagttcaggaaacactcgccacatagcatt 1616
TTGTTGGGTTTTTCTGACTCCAAGAAAGGCTGCTTGAAATGATCGATAC 536	1734	
	Oy 1617 CCAT           Db 1794 CCAT	CCATGGGAGTATGTCCTGCAAAACTGGATTGGATTGGAGCATTATTCGATCATTAGCTAT 1676 
AIGGICCGGCCAAAGIAAICIGIGIIIGIIGGGAIGGGIGGIITAGGGAA 773 CGAGGAAQATCTTTGAAAGCGAAGAACATTAGGAAGAACATTCCCTTG 656	Qy 1677 TTTT      Db 1854 TTTT	TTTTGGTGACCGAAGAGTCTAGCACTGCAGTTTGTCCAGATCAATTGAGGATGTT 1736 
CGAGGAAGATCTTTGAAAGCGAAGAAGACATTAGGAAGAACTTCCCTTG 833 ITACAGTGTCACAATCATTCACAGGATTGAGCTACTTAAAGATATGAT 716	1737	ACGGGTCTTGGATCTTGAAGATGTGACATTCTTAATCACTCAAAAAGATTTCGACCGTAT 1796
	1914	
TTGGCCCCAGTTCTCTGGATCAACTCTTGCAAGAATTGCAAGGGAAGGT 776	Oy 1797 TGCA             Db 1974 TGCA	TGCATTGTTGTGCCCATTGAAATACTTGAGTATTGGATATTCGTCATCCATATATACAT 1856 
	Oy 1857 TCCC           Db 2034 TCCC	TCCCAGATCCATTGGTAAACTACAGGGCCTACAAACTTTGAACATGCCGAGCACATACAT
IACATCATCTTTCTGAGTACCTGATAGAAGAGCTCAAGGAGAAGAGGTA 1013 TAGATGATCTATGGATTTTACATGATTGGAATTGGATAAATGAAATTGC 896	Qy 1917 TGCA	TGCAGCACTACCAAGTGAGATCAGTAAACTCCAATGTCTGCATACTCTTCGTTGTATAGG 1976

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The invention comprises the amino acid and coding sequences of nucleotide binding site (NBS) proteins from the Oryza minuta Pi9 locus (bacterial blight and rice blast resistance genes). The DNA sequences may be used as markers for resistance to infection with Manaporthe grises in plant breeding programs. The present DNA sequence represents the Oryza minuta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTGAAGAAGTGAGTAGCAGGAACACGCTACAGTTTAGTCAAGCCTATTTCCTCTGGCA 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, Nand NBS3, useful for producing plants resistant to Magnaporthe grisea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 76272 BP; 22112 A; 16049 C; 16316 G; 21795 T; 0 U; 0 Other;
                                                                                                                                                                                                                     nucleotide binding site; NBS; Pi9; bacterial blight; rice blast; plant breeding; transgenic plant; plant; ds.
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                           Oryza minuta Pi9 locus genomic DNA sequence.
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                                                                                                            ADI57166 standard; DNA; 76272
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01-FEB-2002; 2002US-0353304P.
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97.1%;
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Matches 2872; Conserv
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                         2214 ATGCCTGCCTAAAGTATTCACACCTTTAGTTAGTCGCGATGATGCTGGCAAAACAAATTGC
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                                                                                                                         The invention relates to novel broad-spectrum resistance gene Pi2 and the NSS(1-6) genes present in the Pi2 gene cluster region. The rice Pi2-like disease resistance nucleic acid molecules are useful for enhancing disease resistance in plants. The present sequence represents a cDNA
                                confers
                               molecule that confers
or enhancing disease
                                                                                                                                                                                                                                                                                                                                     CTGAGCTTGTTGGGGTTTTCTGACTCCAAGAAAAGGCTGCTTGAAATGATGGTGCAATG
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                                                                                                                                                                                                                                                   77.2%; Score 2393.6; DB 12;
llarity 96.1%; Pred. No. 0;
Conservative 0; Mismatches 99; I.
                               nucleic acid
for creating
                                                                                           Claim 1; SEQ ID NO 11; 120pp; English
                             Pi2-like disease resistance resistance in plants, useful
                                                                                                                                                                                       encoding a rice NBS6 polypeptide.
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P-PSDB; ADM72249
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                                                                                                                                               The invention relates to novel broad-spectrum resistance gene Pi2 and the MBS(1-6) genes present in the Pi2 gene cluster region. The rice Pi2-like disease resistance nucleic acid molecules are useful for enhancing disease resistance in plants. The present sequence represents a cDNA-21 fragment from the Pi2 region, that matched to NBS4.
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Pred. No. 0;
nucleotide binding site; NBS; Pi9 gene; bacterial blight; rice plant breeding; transgenic plant; plant; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 763; Indels
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01-FEB-2002; 2002US-0353304P.
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Best Local Similarity 72.6
Matches 2168; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids
and NBS3, usef
                                                                                  Oryza minuta
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2619 AAATGGGAGCATTCCCAAATCTTAGAACATTTTCGATTTACAATTTGGAGCAGCTAAGAG 2678
                                                                                                                                                                                              The invention comprises the amino acid and coding sequences of nucleotide binding site (NBS) proteins from the Oryza minuta Pi9 locus (bacterial blight and rice blast resistance genes). The DNA sequences may be used as markers for resistance to infection with Magnaporthe grisea in plant breeding programs. The present DNA sequence represents an NBS gene from the Oryza minuta Pi9 locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2 and NBS3, useful for producing plants resistant to Magnaporthe grisea
                                                                                      GGTTGGAATCAGGGATTGTTGGTATCATTCACCTTCCAAGGCTCAAGGAGTTTCACCTTG
                         AGATCAGATTTGAGGACGCCAGCTCACCCCTGTTGGAAAAGATAGAAATAGGCGAGTGCA
                                    GGTTGGAATCTGGGATTACTGGTATCATCACCTTCCAAAGCTCAAAGAGAGATTCCAATTA
                                                                                                                                                 GATACGGAAGTAAAGTGGCTAGGCTTGGTCAGCTGGAGGGAAGTGCGCACACACCCAA
                                                                                                                                                                      ATCGCCCCGTGCTGCTAATGTACAGTGACCGAAGGTATCACGACCTGGGGGCTGAAGCCG
                                                                                                                        nucleotide binding site; NBS; Pi9 gene; bacterial blight; rice blast; plant breeding; transgenic plant; plant; gene; ds.
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Pred. No. 0;
0; Mismatches 818; Indels
                                                                                                                                                                                                                                                                                                                                                                                  binding site (NBS)
                                                                                                                                                                                                                        2921 AAGGATCTTCTATAGAAGTGCAAACAGCAGATCCTGT 2957
                                                                                                                                                                                                                                     AAGGATCCCCTGTTGAAGTGGAAGCAACAGATCCTGT 2951
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01-FEB-2002; 2002US-0353304P.
                                                                                                                                                                                                                                                                                                           standard; DNA; 2940
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Best Local Similarity 71.7%;
Matches 2092; Conservative
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P-PSDB; ADI57168.
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LIU G.
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                                                                                                                                                 THACGGGTCTTGGATCTAACAGATGCACAATTTTCTATCACAAAATGATGTCGACAAC 1794
                                                                                                                                                                                    ATTGCATTGTTGTGCCACTTGAAATACTTGAGTATT------GGATATTCGTCATC 1844
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                                                                                                                                                                                                                                                                                          The invention relates to novel broad-spectrum resistance gene Pi2 and the NBS(1-6) genes present in the Pi2 gene cluster region. The rice Pi2-like disease resistance nucleic acid molecules are useful for enhancing disease resistance in plants. The present sequence represents a cDNA
                                                                                                                                                                                                               molecule that confers
or enhancing disease
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                                                                                                                                                                                                              New rice Pi2-like disease resistance nucleic acid disease resistance in plants, useful for creating resistance in plants.
                                                                                                                                                                                                                                                                                                                                                                                                  50.1%; Score 1553.4; ilarity 71.5%; Pred. No. 0; Conservative 0; Mismatches
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                                              GATTCCCTTGATGAATTTAAGGTCCATATTGAAAGCCAAACCCTATTTCGTCAGTTGGTG
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0; Mismatches 932;
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01-FEB-2002; 2002US-0353304P.
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2746 GAATCTGGGATTACTGGTATCATTCACCTTCCAAAGCTCAAGGAGATTCCAATTAGATAC
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18-MAR-2003; 2003US-0455713P.
05-SEP-2003; 2003US-00656394.
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                                                                                                                                      The invention relates to novel broad-spectrum resistance gene Pi2 and the NBS(1-6) genes present in the Pi2 gene cluster region. The rice Pi2-like disease resistance nucleic acid molecules are useful for enhancing disease resistance in plants. The present sequence represents a cDNA encoding a rice NBS3 polypeptide.
                                                                                                                                                                                                                                                                                                                        9
                                                              molecule that confers
or enhancing disease
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                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                            Score 1040.4; DB 12; Length 4147; Pred. No. 3.4e-284; 0; Mismatches 641; Indels 37; 0
                                                                                                                                                                                                                     Sequence 4147 BP; 1201 A; 831 C; 1029 G; 1086 T; 0 U; 0 Other;
                                                              nucleic acid
for creating
                                                                                                                 Example 4; SEQ ID NO 5; 120pp; English.
                                                              resistance in plants, useful
                                                                                                                                                                                                                                              33.6%;
                                                                 New rice Pi2-like disease
                                                                                                                                                                                                                                                          Best Local Similarity 69.2
Matches 1522; Conservative
                                                                                          resistance in plants
                          2004-257576/24
                                        P-PSDB; ADM72243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2 and NBS3, useful for producing plants resistant to Magnaporthe grisea
                                                                cagacgracaritrcaacacreccaacreagarracr-aacrregagrerecgragecrr
                                                                                       CGTTGTATAGGACAGTTTCATTATGACAACTTTAGTCTAAACCACCCAATGAAGTGCATA
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                                                                                                                                                                                                                                                                                                                                                                                                  ing site; NBS; Pi9; bacterial blight; rice blast; transgenic plant; plant; ds.
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                                                                                                                                                                                                                                                                                                                                                                              sequence #1
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           Indels
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0; Mismatches 52;
 94.8%;
Similarity 94.6
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Length 2265;

DB 12;

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Query Match

Sequence 2265 BP; 638 A; 471 C; 558 G; 598 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2 and NBS3, useful for producing plants resistant to Magnaporthe grisea
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                                                                                                                     Pi9; bacterial blight, rice blast;
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Pred. No. 7.6e-227;
0; Mismatches 573;
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                                                                                                                                      plant breeding; transgenic plant; plant; ds
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                                                                                              Oryza minuta Pi9 locus-related DNA
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01-FEB-2002; 2002US-0353304P.
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Db 1439 ACTTGCAGAATAGCCAACTAGAGAGGAGAAACAATGGAGAACTCGCCTA 1498

Oy 2564 ACCTCATGCTCATCTTTATCGGAATGCTTGCGGAGAACTCGCCTA 1498

1499 ATCTCATGCTCCTTTATCGGAATGCTTGCGGAGAGCTGGTTTCAGGG 1558

Oy 2624 CAGAGCATTCCTTAGTTGGCGGGGGAAGCTGGTGTTTCAGGG 1558

Db 1559 AGGACATTCCCAATCTTAGAACCTTTGGATTTATGAATTGGATCAGTAGAGAG 2683

1559 AGGAGCATTCCCAATCTTAGAACCTTTGGATTTATGAATTGGATCAGTAAGAGGG 1618

Oy 2684 TCAGATTTGAGACGGCAGCTCCCCTTGGATTGAATTGGATCAGACTGAAGAGG 1618

Oy 2684 TCAGATTTGAGACGGCAGCTCCCCCTTGGATTGAATAGAATAGCAGATTGAGT 1678

Db 1619 TGAGATTTGAGGGGAACCTCACCCTGGATGGAATGAAATAGCAGATTCAATTAGAT 2803

1619 TGAGATTTGAGGGGAACCTCACCCTGGATGGAAAGGTTCAATAGATATTAGAT 2803

Oy 2804 ACGGAAGTAGTGGGATTCATTCACTTCCAAAGGTTTCACTTGAAT 1738

Oy ACGGAAGTAGTAGGGGAGCTTGGAAGGTTAAGGAGATTCACTTGAAT 1738

Oy 2804 ACGGAAGTAAGTGAGGCTTGGAAGGTTAAGGAGAATCCCAATC 1798

Oy 2804 ACGGAAGTAATGTACAACTGCTAGAGTTAAGGAGAATCACCCCAATC 1798

Oy 2804 ACGGAAGTAATGTACAAGGCTAGAGGTTAAATGGGCACACCCCAATC 1798

Oy 2804 ACGGAAGTAATGTACAAGGCTAGAGGTTAAATGGGCACACCCCAATC 1798

Oy 2804 ACGGAAGTGATGGAAGGTACCGAAGGTTAAATGGGCACACCCCAATC 1798

Oy 2804 ACGGAAGTGCTAAAGTGACCGAAGGTTAAAGGGCACACCCCAATC 1798

Oy CCCCCGTGCTGCTGAATGTACAGACCTAGAGGTTAAATGGGCACACCCCAATC 1798

Oy GCCCCTGTGCTGAATGTACGGACCCCAAGGTTAACACACCTGGGG 2910

DD 1739 GACCCCTTTAGGACTAGGTCACCCTAGGGG 1845
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Search completed: February 12, 2005, 23:55:52 Job time : 1050.76 secs

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CL964072 OSIFCCO10
CL963354 OSIFCCO10
CL963164 OSIFCCO10
AG210016 Oryza sat
CF015622 FB1 17 D1
CL812740 OR CBa005
CL85832 OR CBa005
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CL847958 SCEZRZ101
CW518670 OP Ba002
AQ578469 hbxbb0093A
CL197270 104 424 1
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CL582775 OB Ba004
AB155403 Oryza sat
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Listing first 45 summaries
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REFI	REFERENCE AUTHORS	Ehrh 1 (I Ma,L	hartoideae; Oryzeae; (bases 1 to 3159) L., Wangc,J., Chen,C o,Y., Sun,N., Zhang,	3e; Or to 31 c,J.;	Syze Che Zha	Ehrhartoideae; Oryzeae; Oryza. 1 (bases 1 to 3159) Ma,L., Wangc,J., Chen,C., Liu,X., Su, Jao,Y., Sun,N., Zhang,X., Bao,J., Su	N., Li,L., Wang,X., n,D., Zhao,H., Yuan	Cao, M.,
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Chinese Academy of Sciences, Beijing 101300, China Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
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Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Benhartoideae, Oryzae, Streptophyta, Enthartoideae, Oryzae, Oryza, Liliopsida, Poales, Poaceae, Enthartoideae, Oryzae, Oryza, Manot., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Jao, Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J.
Manalysis of transcriptional regulation of the rice genome and the comparison to Arabidopsis
                CTTCATCTTTATCGGAATGCTTACCTTGGGGAGAAGCTAGTATTCAAAACAGGAGCATTC
                                                                               TCCCTCCAATCTCTCCATGTGGATGCTGCAGGAATCTCAGATGGTGGAACACTTGAGTGC
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Department of Bioinformatic
Beijing Institute of Genomics
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Enthartoideae; Oryzae; Oryza.

Enthartoideae; Oryzae; Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Mang,X., Engy,X., and Wang,J.

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 OsIFCCO09286 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
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|mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                         Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
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65.2%; Pred. No. 0;
iive 0; Mismatches 964;
                                                                                                                                                                                                                                                                                                                                                                                             Email: chenchen@genomics.org.cn
                                                                                                                                                                                                                                                                                                                                                                                                                              Class: exon-trapped.
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662 bp DNA linear GSS 09-AUG-2003 Oryza sativa (japonica cultivar-group) DNA, clone:WE9007 0 102 1A, 3' flanking sequence of Tos17 insertion in rice strain NE9007, AG210016 Survey sequence.
                                                                                                                                                                                                                                                                    GAGATTCCAATTAGATACGGAAGTAAAGTGGCTGGGCTTGGTCAGCTGGAGGAGAAGTG 2847
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota, Viridiplantea; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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[Oryza sativa (japonica cultivar-group)] (BAA90798.1)."
                                                                                                                                                                        ATAGGCGAGTGCAGGTTGGAATCTGGGATTACTGGTATCATTCACCTTCCAAAGCTCAAG
2668 GATCAGCTAAGAGAGATCAGATTTGAGGACGGCAGCTCACCCCTGTTGGAAAAGATAGAA
                                      TCCGAACTAAGAGGGATAAGATTTGAGAAGGACGCCTTGCCCCACATGGAAAGAATGGAA
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Miyao,A., Tanaka,K. and Hirochika,H.
Miyao,A., Tanaka,K. and Hirochika,H.
Direct Submission
Submitted (16-APR-2002) Akio Miyao, National Institute of
Agrobiological Sciences, Molecular Genetics; 2-1-2, Kannondai,
Tsukuba, Ibaraki 305-8602, Japan (E-mail:miyao@affrc.go.jp,
URL:http://cos.nias.affrc.go.jp/, Tel:81-298-38-7020,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:39947"
/db_xref="taxon:39947"
/db_xref="taxon:39947"
/dbo=1185007 0_102_1A"
/clone lib="PCR product directly amplified from rice genomic DNA"
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Target Site Specificity of the Tos17 Retrotransposon Shows a Preference for Insertion within Genes and against Insertion in the Carl Service State Regions of the Genome Plant Cell 15 (8), 1771-1780 (2003)
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AUTHORS Miyao,A., Murata,K. and Hirochika,H.  TITLE Direct Submission JOURNAL Submitted (16.APR-2002) Akio Miyao, National Institute of Agrobiological Sciences, Molecular Genetics; 2-1-2, Kannondai, Tsukuba, Ibaraki 316-8602, Japan (E-mail:miyao@affrc.go.jp, URL:http://tos.nias.affrc.go.jp/, Tel:81-298-38-7020, Fax:81-298-38-7020) FEATURES Location/Qualifiers   /organism="Orza sativa (japonica cultivar-group)"     // mol_type="genomic DNA"     // clivar="Nipponbare"     // cl	/clone_lib="PCR product directly amplified from rice genomic_DNA" //note="The 3' end of retrotransposon Tosl7 was found immediately upstream of this sequence."  ORIGIN Query Match 16.1%; Score 497.4; DB 9; Length 698; Best Local Similarity 85.7%; Pred. No. 2.4e-127; Matches 552; Conservative 0; Mismatches 92; Indels 0; Gaps 0;		Db 121 TCTCCCTATTGAGGACACTCAGGTTGAAGGGTTGAAGAGTTGCCTAACTGGAT 180  Qy 2475 TGAGCAGCTCACTCACAGAGAAGATCTATTGAGGAGCAAACTAAGGAAGG	<u> </u>
0y         2262 ATTAGGTGTGACAACAGGAAAATGTAAGTAAGTTATGCAGCCAT         2321           1 ATTAGGTGTGACAACAAAGGAAAAATGTAAGTTATGCAGCCAT         50           2322 TGAGAAGTCTCTCCCTCCAATCTCTCCATGTGGATGCTTATTCTCAGGTATTATT         60           2322 TGAGAAGCTCTTCCCTCCAATCTCTCCCATGTGGATGCTTATTCTCAGGTATTAT         120           0y         2379 TGGAACACTTGAGTGCCTAGATTCTATTTCATCTCCTCCTCTCTCT		Qy         2619 CAAAACAGGAGCATTCCCAAATCTTAGAACACTTTAGATTATGAATTGGATCAGCTAAG 2678           Db         361 CAAAACGGAGCATTCCCAAATCTTAGAACATTTATATTAGAATCAGCTAAG 420           Db         2679 AGAGATCAGATTCCCAAATTTAGAACACTTTGTATTTAGAATTAGATCAGCTAAG 420           Db         421 AGAATCAGATTTGGAACACCTCCCCTGTTGGAAAGATTAGAATAGGCAAGTG 2738           Db         421 AGAATCAGATTATTGGAACCCCCTGTTGGAAAAGATAGAATTCCAAAGTG 480           QY         2739 CAGGTTGGAATCTGGCAATCATTCACTTCCAAAGCTCAAAGAATTCCAAT 2798           Db         481 CAGGTTGGAATTATTGGTATCATTCACCTTCCAAAGGCTCAAGGAATTCCAAT 540	QY         2799 TAGATACGGAAGTAAAGTGGCTGGGCTTGGTCAGCTGGAGGAGAAGTGAACGCACCCC         2858           Db         541 TACATACGGAAGTAAAGTGGCTGGGCTTGGTCAGCTGGAGGAGAAGTGAACACACCCC         600           QY         2859 AAATCGCCCCGTGCTGCTAATGTACAGTGA-CCGAAGGTATCACGACCTGGGGGCTGAAG         2917           Db         601 AAATCGCCCCGTGCTGCTAATGTACAGTGA-CCCGAAGGTATCACGACCTGGGGGCTGAAG         600           QY         2918 CC         2919           Db         661 CC         662	RESULT 5 AG208890 LOCUS LOCUS LOCUS AG208890 LOCYZA SALIVA (japonica cultivar-group) DNA, clone:NE4506_0_401_1A, 3' flanking sequence of Tos17 insertion in rice strain NE4506, ACCESSION VERSION REYWORDS COTYZA SALIVA (japonica cultivar-group) COTYZA SALIVA (japonica cultivar-group) COTYZA SALIVA (japonica cultivar-group) BURATYOTA; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Ehrhartoideae; Oryzaa Nyao, A., Tanaka, K., Manata, K., Sawaki, H., Takeda, S., Abe, K., Shinozuka, Y., Ohosato, K. and Hirochika, H. TITLE Target Site Specificity of the Tos17 Retrotransposon Shows a Preference for Insertion within Genes and against Insertion in Pubmed 12877294  REFERENCE 2 (bases 1 to 698)

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OR_CBa0055J06.r OR_CBa Oryza rufipogon genomic clone OR_CBa0055J06
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrhartoideae; Oryzae; Oryza.
1 (bases 1 to 703)
Kim,H., Yu,Y., Wissotski,M., Yost,D., Stum,D., Rao,K., Luo,M.,
Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and
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Unpublished (2004)
Contract: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Porbes Building Room 303, Tucson, AZ 85721-0036, USA
Fax: 520 621 1259
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1. .703
/organism="Oryza rufipogon"
/mol_type="genomic DN4"
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/dlohe="FB1 17 D11 A002"
/lab_host="DH108-T1 phage-resistant E. coli"
/lab_host="DH108-T1 phage-resistant E. coli"
/clone lib="Iron-deficient seedlings"
/clone lib="Iron-deficient seedlings"
/note="Vector: pME18S-FL3; Site_1: Xho1; Site_2: Xho1; The library was prepared from polyA+ RNA from seedlings grown hydroponically and in the absence of added iron. At 8 days of age, roots and shoots ware harvested and stored at -80 C until RNA was isolated. Double-stranded cDNA was cloned unidirectionally into different Dralli sites of the pME18S-FL3 vector (5-prime Dralli site is CACTGTGTG; 3-prime DrallI site is CACTGTGTG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mmpratt@qqq .edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & W University;
Sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
exclude polyA.
                                                                                                                                                                                                                                                                                 Liang, C.,
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                                                                                                                                                                            Eukāryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                       S Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C Sun, F., Sullivan, R., Harris, K., Eastman, A. and Pratt, L.H. An EST database from Sorghum: iron-deficient seedlings Unpublished (2003)
Cother ESTS: FEL 17 D11.bl A002
Cother ESTS: FEL 17 D11.bl A002
Cottact: Cordonnier-Pratt MM
Laboratory for Genomier-Pratt MM
Laboratory for Genomies and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 583 0210
17 D11.gl A002 Iron-deficient seedlings Sorghum bicolor cDNA PFEL_17_D11_A002 5', mRNA sequence.
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llarity 74.1%; Pred. No. 6.8e-109;
Conservative 0; Mismatches 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: Sug5 (CTTCTGCTCTAAAAGCTGCG)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'organism="Sorghum bicolor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/cultivar="BTx623"
                                                                                                                              Sorghum bicolor (sorghum)
Sorghum bicolor
                                                                             CF071622.1 GI:33108281
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/mol_type="genomic DNA"
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/dev_stage="2 week old seedlings"
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/clone_lib="OR_CBa"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII;
drk treated 36 hrs before harvest"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298 ATTTGACAGGAAAGAAATTCTGAAACAAATGATCAGGCAACTTCTGGGTGCTGATTCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         744 GGATCAACTCTTGCAAGAATTGCAAGGGAAGGTGGTGGTGCAAGTACATCATCTTTCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  358 agacaaacricirigaaagaarriragrgagaacrigcriccrigcaagrccagcarcrigg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        387 CAGTTTAGTCAAGCCTATTTCCTCT---GGCACAGAGATTGACATGGATTCCTATGCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCCAAGAAAAGGCTGCTTGAAATGATCGATACCAATGCTAATGATGGTCCGGCCAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 GACTAAAGATGATTGCTTAAACTGATAGATGTCAATACTAATGACGGTCCAGCTAAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          564 AATCTGTGTTGTGGGATGGGTGTTTAGGCAAGACAGCTCTTTCGAGGAAGATCTTTGA
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  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 737)
Kim, H., Yu, Y., Wissotski, M., Yost, D., Stum, D., Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and
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                                                                                                                                                                                                                                                                85721-0036, USA
                                                                                                                                                                                                                                 University of Arizona
Porbes Building Room 303, Tucson, AZ 85:
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
PCR PRimers
FORWARD: TAA TAC GAC TCA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Place: 0009 Frow: H column: 17
Seq primer: TAA TAC GAC TCA TAG GG
Class: BAC ends.
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    .737
    organism="Oryza rufipogon"

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                                                                                                                                            OMAR project
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
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Matches 516; Conserv
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/clone="OR_CBa0055J06"
/tissue type="young leaves"
/dev stage="young leaves"
/dev stage="2 week old seedlings"
/lab_host="DH10B T1 phage resistent"
/clone llb="OR_CBa"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII;
drk treated 36 hrs before harvest"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGATACTTTATGCAGCCATTGAGAAGCTCTCTTCCCTCCAATCTCTCCATGTGGATGCTG 2362
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Oryza rufipogon
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2123 GCTGGTCTGAATCAATCGGTGTGAAGGTACCCAAAGGAATAGGTAAGTTGCGAGACTTGC
                                                                                                                                                                                                                                                                                                                                                     GTTGGTCTGATACAAAGGGTGTGAGGGTGTCAAGAGGAATTGACAACCTAAAAGAGTTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                     638 AGATTCTAGAAGTCGTGGACATCAACAGAACTAGTAGGAAGGCGATTGAAGAGCTGGGGG
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                                                                                                                                                                                                             Length 703;
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Best Local Similarity 72.7
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683 297 743 357 803

683 297 743 803 417

563 180 623 923

537

983 597 657

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Saccharum officinarum
Bukaryota; Viridiplantea; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Spermatophyta; Magnoliophyta; Saccharum; Saccharum officinarum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CA147958 709 bp mRNA linear EST 24-SEP-2003
SCEZERZL015C04.g RZ1 Saccharum officinarum cDNA clone SCEZERZ1015C04
5/, mRNA sequence.
CA147958
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                                                                                                                                                                                241 AAACAAGGAACACAT---GAAGAACTTCTCGTGTTGTGCTTGGATCACTGTGTCTCAGTC
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AGACATTCGTAATCAGTCAGCTCGCAATGTGGATGAGGCTGAGCTTGTTGGGTTTTCTGA
                                                                           504 CTCCAAGAAAAGGCTGCTTGAAATGATCGATACCAATGCTAATGATGGTCCGGCCAAGGT
                                                                                                564 AATCTGTGTTGTTGGGATGGGTGGTTTAGGCAAGACAGCTCTTTCGAGGAAGATCTTTGA
                                                                                                                                                                                                                                   624 AAGCGAAGAAGACATTAGGAAGAACTTCCCTTGCAATGCTTGGATTACAGTGTCACAATC
                                                                                                                                                                                                                                                                                                                 ATTICACAGGATIGAGCIACTIAAAGATAIGATACGCCAACTICTIGGCCCCCAGTICTCT
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Contact: Arruda P
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Universidade Estadual de Campinas
Caixa Postal 610, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
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1 (bases 1 to 709)
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CA147958
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CCBa0093P17.f OR_CBa Oryza rufipogon genomic clone OR_CBa0093P17
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                                                                                                                                                     598 TATTTACCACCTTGAACCGTTACATATAGATGATGCTATACACTTGCTACTAGCAAAGAC 657
                                                                                                                                                                                                                                   658 AAACATAAGACTTGAAGACATGGAAAATGATGAGGACTTGGGCAGCATAGTTACAAAATT 717
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.

1 (bases 1 to 740)
Kim,H., Yu,Y., Wissotski,M., Yost,D., Stum,D., Rao,K., Luo,M.,
Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and
478 CATAGATGCATGGAATTGGATTCATGATATTGCTTTTCCGAAGATTAACAACAGGGTAG 537
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                                      TCGAATAGTAATAACCACTCGGAATGTTGATCTTGCGGAGAAGTGTGCCACAGCCTCACT
                                                                           538 recentantantaneacacacagarecreserraseresanesistacererantate
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Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Forbes 1520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
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/mol_type="genomic DNA"
/mol_type="genomic DNA"
/db_xref="taxon:4529"
/clone="OR CBa0093P1"
/tissue_type="young leaves"
/dev_etage="2" week old seedlings"
/lab host="DH10B T1 phage resistant"
/clone_lib="OR_CBa"
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BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0093 row: P column: 17
Seg primer: TAA TAC GAC TCA TAG
Class: BAC ends.
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CL861885
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OMAP project
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
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                                                                                                                                                                                                                                                                                                                 718 GGTAAAAGGGTGTGGT 733
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OF SOURCE OF BAOUSSOUS.r OP BA Oryza punctata genomic clone OP Ba0025003 33, genomic survey sequence. CW518670
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Basecalling by phred version 0.020425.c. This sequence was derived
from the raw sequence read by clipping with lucy version 1.19s.
Bases 119-993 of the raw sequence (length 1389) were retained after
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Oryza punctata"
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/db xref='taxon:4537"
/db xref='taxon:4537"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotes, Varidiplantae; Streptophyta; Embryophyta, Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Enrhartoideae; Oryzeae; Oryzea.

1 (bases 1 to 875)
SanMiguel, P., Westerman, R., Kim, H., Yu, Y., Wissotski, M., Yost, D., Stum, D., Rao, K., Luo, M., Jettry, R., Kudrna, D., Muller, C., Matfield, J., Soderlund, C., Wing, R. and Jackson, S.A.

Omap Project - Purdue University
Unpublished (2004)
Contact: Scott A. Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          668 TIACAGTGTCACAATCATITCACAGGATTGAGCTACTIAAAGATATGATACGCCAACTIC 727
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                                                                              2843 AAGTGAACGCACACCCCAAATCGCCCCGTGCTGCTAATGTACAGTGACCGAAG 2894
                                                                                                                        AAGTGAACGCACACCCCAATCATCCTGTCCTGGGGCTGGTACATGACCGAAG 709
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Tel: 7654963621
Fax: 7654967255
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BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 161000 Std Brror: 0.00
Plate: 10055 row: O column: 03
Seg primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone lib="RZI"
/clone lib="RZI"
/clone lib="RZI"
/note="Organ: Shoot-root transition zone from young plants
(large insert library); Vector: pSporti; Site 1: SalI;
Site 2: NotI; An unidirectional cDNA library generated
from [Shoot-root transition zone from young plants (large
insert library)]. CDNA was prepared from polyA+ mRNA
using SuperScript plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://sucest.lad.ic.unicamp.br/public"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAGAAATCAGGCGCTGCATTTTGAAGTCAGGGATTATTGGCATCAAGCACCTTCCAAGGC 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 TTACACAGCTGGTGAAGATTTCCTTAATCTGTAGCCAGCTAAAGGAAGATAAAACCATGG 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2363 CAGGAATCTCAGAIGGIGGAACACTIGAGAGACTCTATTTCAICTCCTCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2183 AGGTTCTAGAGTATGTAGATATCAGGCGGACCAGTAGTAGAGGCAATCAAAGAGCTGGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AGATACTAGAGTCTGTGGACATTAGAAGAACTAGCAGCAAAGCAGTTAAAGAGCTCGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCTGACCCGATTAAGAAACTAGCCACTGGAACAAACGGGGCTTCCAAGAAAAGTGTA
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Email: parruda@unicamp.br
Clone distribution: clone distribution information can be through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br
Plate: 015 row: C column: 04
Seq primer: T7 Promoter Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.6%; Score 358.4; DB 6; Length 709; 69.9%; Pred. No. 2.1e-88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 211; Indels
                                                                                                                                                                                                                                                           1. .709
| forganism="Saccharum officinarum" |
| forganism="Raccharum officinarum" |
| forganism="Raccharum officinarum" |
| forganism="Sccarzioliscom" |
| forganism="Saccharum officioliscom" |
| forganism="Saccharum officioli
                                                                                                                                                                                                                                                                                                                                                                                                                                               lab host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 498; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2423
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/tissue type="Leaf"
//tissue type="Leaf"
/lab_host="Leaf"
/lab_host="Leaf"
/lab_host="E. coli DH10B"
/clone llb="CdGI Rice BAC Library"
/note="Vector: pBe10BAC11; Site 1: HindIII; Site 2:
/note="Vector: pBe10BAC11; Site 1: HindIII; Site 2:
/note="Vector: pBe10BAC11; Site 1: HindIII; Rice is one of two most popular grains In the world half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1173 GTCAGAATGGGAGAAATTCTATGAACACCTTCCTTCAGAACTAGAAATAAACCCAAGCCT 1232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1233 GGAAGCTTTGAGGAGAATGGTGACCCTAGGTTACAACCACCTACCATCCCATTTGAAACC 1292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1293 ATG-CTTTTTGTATCTAAGTATCTTTCCTGAGGATTTTTGAAATCAAAAGGAATCGTCTAG 1351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       410 TGAAGCAATGGAAAGGATAGTGACCCTAAGTTACAACTACTTGCCATCTCATCTTAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              crrradacccrrcadarradacrarideadagagrracrrcradagaaagccaarradac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1352 TAGGTAGATGGATAGCAGAAGGGTTTGTTAGACCAAAGGTTGGGATGACGACTAAGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAAATAGATGGATGGCAGAGGGGTTTATTAAAGCTAGGGCTAATATGACTATTGAAGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230 TTGGGAAAAGTTACTTTAAAGAACTCATCAACCGTAGCATGATTCAGCCATCAAGAGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCATAGCAGGAAAATTAAGACTTGTCGAATTCATGATATCATCGTGATATCACAGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CACAGAAGATATAGGAAGGGATTAAAAGATGAGTGACATTATTACTAANATAGTAAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1113 ATGTGGTCGTCTACCATTAGCAATACTTACAATAGGAGCTGTGCTTGCAACTAAACAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               470 AAAAGAGIGGGAAACCITITATAGICAGATACCITCAGAGCTIGAAAGCAACCAAACCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1053 TCATGAAGACATGGAATCAAATAAAAATATGCAAAAGATGGTTGAACGAATTGTAAATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                              /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the whole library for colony screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.4%; Score 352.6; DB 8; Similarity 72.7%; Pred. No. 8.5e-87; B; Conservative 0; Mismatches 175;
Seg primer: GGAAACAGCTATGACCATG
Class: BAC ends
High quality sequence stop: 224.
Location/Qualifiers
                                                                                                                                                                                     /db xref="taxon:39947"
/clone="nbxb0093A15r"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Simi
Matches 468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                530
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                                                                     FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGAACTAGAAATAAACCCAAG-CCTGGAAGCTTTGAGGAGAATGGTGACCCTAGGTTAC 1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACCACCTACCATCCCATTTGAAACCATGCTTTTTGTATCTAAGTATCTTTCCTGAGGAT 1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSS 02-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             657
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                                                                       787
                                                                                                                  297
                                                                                                                                                                                                                                                           848 TAGATGATCTATGGATTTTACATGATTGGAATTGGATAAATGAAATTGCATTTCCTAAGA 907
                                                                                                                                                                                                                                                                                        967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGAGCTTGAGAGCAACCCAAGCCTCGAAGCATAAAGGAGGGTGGTGACCCTAAGCTAT 777
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bormatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 663)
                                                                                                                                                                                                           298 TACCTGACGTTGGTACTTACCTGCAAATCGGCTGAAAGAATTGAGGTACTTTGTTGTTTT 357
TIGTTGTGTCACAGTCATTTTCGAAGATAGAGATGCTCAAAGATATGATTAGCCAACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               598 GCATAGTTACACAATTAGTTAAAAAGTGTGGCCGTTTACCACTGGCCCATAGTAACGATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      778 GACCATTTTGCATCTCATCTTAAGCCATGCTTTCTATACCTAAGCATTTTTTCTTGAGAT
                                                                       TTGGCCCCAGTTCTCTGGATCAACTCTTGCAAGAATTGCAAGGGAAGGTGGTGCTAG
                                                                                                                  TAGGTCCTAATTCATTGAAGGAATGCTTGAAAGGGCTTGAAGGGAA---GGCAATGCAAG
                                                                                                                                                                  TACATCATCTTTCTGAGTACCTGATAGAAGAGCTCAAGGAGAAGAGGTACTTTGTTGTTC
                                                                                                                                                                                                                                                                                                                                                   908 ACAATAAGAAGGCCAGTCGAATAGTAATAACCACTCGGAATGTTGATCTTGCGGAGAAGT
                                                                                                                                                                                                                                                                                                                                                                                               418 CAAACAACAAAGGGGTCGGGTAATAGTAACAACTAGATTAGATGGTGTAGCTAATGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         478 GCACTACTGAACCATATGTCTACCGCCTTAAACTCCTAGAGATTGAGTGTGCCATAGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGCAATGTTTGCTAATAAACATTCATCAAGTGGGAAGAAATGTGCAGCCAACTTCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nbxb0093A15r CUGI Rice BAC Library Oryza sativa (japonica cultivar-group) genomic clone nbxb0093A15r, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Rice
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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Clemson University
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Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
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CL197270 603 bp DNA linear GSS 06-JAN-2004 104 424 10943635 114 32333 078 Sorghum methylation-filtered library (LibID: 104) Sorghum bicolor genomic clone 10943635, genomic survey
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Sorghum bicolor
Sorghum bicolor
Sorghum bicolor
Sorghum bicolor
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD
clade; Panicoldeae; Andropogoneae; Sorghum.

1 (bases 1 to 603)
Budiman, M.A., Pilck, E., Jones, J., Nunberg, A., Citek, R.W.,
Robbins, D., Rohlfing, T., Bradford, K., Fries, J., McMenamy, J.,
Trani, L., Isak, A., Zimmerman, C., Lakey, N. and Bedell, J.A.
GeneThresher methylation filtered genomic sequences from Sorghum
                                           AAGCGAAGAAGACATTAGGAAGAACTTCCCTTGCAATGCTTGGATTACAGTGTCACAATC
                                                                        864 ITTACATGATTGGAATTGGATAAATGAAATTGCATTTCCTAAGAACAATAAGAAGGGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         598 TATTTACCACCTTGAACCGTTACATATAGATGATGCTATACACTTGCTACTAGCAAAGAC
                                                                                                                              684 ATTTCACAGGATTGAGCTACTTAAAGATATGATACGCCAACTTCTTGGCCCCAGTTCTCT
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Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbdell@oriongenomics.com
Plate: 424 row: c column: 19
Seq primer: M13/pUC Forward
Class: shorgun
High quality sequence stop: 603.
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/mol_type="genomic DNA"
/cultivar="ATx623"
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/mol_type="genomic DNA"
/db xref="texon:4529"
/clone="OR_CBa0013H04"
/tissue_type="young leaves"
/dev_stage="2 week old seedlings"
/lab host="Thi0B TI phage resistant"
/clone_lib="OR_CBa"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII;
drk treated 36 hrs before harvest"
                                                                                                                                                                                                                                       CL801486 709 bp DNA linear GSS 06-AUG-2004
OR_CBa0013H04.£ OR_CBa Oryza rufipogon genomic clone OR_CBa0013H04
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1 (bases 1 to 709)

Kim,H., Yu,Y., Wissotski,M., Yost,D., Stum,D., Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and
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                      CAATCTCGAGACAGGAAAATTTTGTATTATTACCAATGGGAGATGGCTCTGATTTAGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
                                                                                 1592 AGGAAACACTCGCCACATAGCATTCCATGGGAGTATGTCCTGC 1635
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BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0013 row: H column: 04
Seg primer: TAA TAC GAC TCA TAG
Class: BAC ends.
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PCR PRimers
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                                                                                                                                                                                                                                                                  5', genomic survey sequence. CL801486
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Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
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/lab host="Jano" or DHSa" /clone lib="WGS-SbicolorF (JM107 adapted methyl filtered)" /clone lib="WGS-SbicolorF (JM107 adapted methyl filtered)" /note="Site 1: Xba I; Site 2: Xba I; The vector was digested with Xbal and one nucleotide was added by fill in in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (.x/y reads in M13mpl9, .b/g reads in µUC19). The same ligation was transformed in either JM107 or DH5a."
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              Rabinowicz_P.D., O'Shaughnessy, A.L., Balija, V., Dedhia, N., Katzenburger, P., King, L., Miller, B., Muller, S., Nascimento, L., Sutavern, T., Palmer, L., McCombie, W.R. and Martienssen, R.A. Genomic shotgun sequences from Sorghum bicolor (methyl-filtered) Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGTIGGGACAACCATIGATGAGGITGGGAAAGAGTACTTIGATGAGCTAATCAGCCGGA
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                                                                                                                 Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Pax: 516 367 8884
Fax: 516 367 8878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 317.6; DB 8;
Pred. No. 5.4e-77;
0; Mismatches 199;
                                                                                                                                                                                                                                                                                                                                                             1. .673
/organism="Sorghum bicolor"
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/clone="ia97a07"
                                                                                                                                                                                                                                                                                                                            quality sequence stop: 673.
Location/Qualifiers
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                                                                                                                                                                                                                                                              Plate: ia97 row: a column:
Seg primer: -21M13UnivFwd
Class: shotgun
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Best Local Similarity 68.5%;
Matches 459; Conservative (
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                                                                           TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAATTGTAAATAAATGTGGTCGTCTACCATTAGCAATACTTACAATAGGAGCTGTGCTTG 1159
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                                                      /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA prepared from purified nuclei was randomly_sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation-filtered library."
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Sorghum bicolor
Sorghum bicolor
Bukaryora, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae; PACCAD
clade, Panicoideae, Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                               9
  'clone="10943635"
| 'clone_lib="Sorghum methylation-filtered library (LibID:
                                                                                                                                                                                                                                                                                                         980 CACTGGTGTACCACCTTGATTTCTTGCAGATGAACGATGCCATAACATTGCTACTGAGAA
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        Qy
        1796 TIGCATTGTGGCACTTGAAATACTTGAGTATTGGTCATCCATATATTCAC 1855

        Db
        543 TAGTGCTGTTGTCTCACTTGAAATATTGGAATATTGGTCATAGAAATCTTACAC 602

        Qy
        1856 TTCCCAGATCCATTGGTAAACTACAGGCCTACAAACTTTGAACATGCCGAGCACATACA 1915

        Db
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        Db
        663 TTACAACCT 672

        Db
        663 TTACAACCCT 672

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        Job time: 6399.15 secs
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Sequence 22, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 157, App
Sequence 157, App
Sequence 157, App
Sequence 157, App
Sequence 213, Appl
Sequence 218, Appl
Sequence 2813, Appl
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Sequence 1813, Ap
Sequence 109, App
Sequence 16369, A
Sequence 7366, Ap
                                      Sequence
Sequence
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APPLICANT: Yano, Masahiro
APPLICANT: Yano, Masahiro
APPLICANT: Katayose, Yuichi
APPLICANT: Katayose, Yuichi
APPLICANT: Sasaki, Takuji
APPLICANT: Yamanouchi, Utako
APPLICANT: Yamanouchi, Utako
APPLICANT: Yamanouchi, Utako
APPLICANT: Ishimaru, Lisa
TITLE OF INVENTION: RICE GENE RESISTANT TO BLAST DISEASE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C
STREET: 225 Franklin Street
CITY: BOSFOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: BC...
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
ZIP: 02110-2804
ZIP: 02110-2804
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: DISACETE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASESED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/330,330
FILING DATE: 11-JUN-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 10-181455
FILING DATE: 12-JUN-1999
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 06501/032001
TELECOMMUNICATION INFORMATION:
TELECHONE: 617/542-5070
TELECHONE: 617/542-6906
TELECHONE: 617/642-6906
US-09-004-838-6

US-09-004-838-2

US-09-806-7088-22

US-08-588-981-15

US-08-986-7088-22

US-08-310-912A-157

US-09-301-085-157

US-09-304-838-128

US-09-004-838-128

US-09-621-976-2813

US-09-621-976-2813

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US-09-949-016-16369

US-09-949-016-16369

US-09-270-767-22648
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478
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6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                                 GenCore version 5.1.6
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US-09-933-170-57

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US-09-933-170-56

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US-09-964-680A-4

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                           February 12, 2005, 22:56:15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                         nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                       IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Sequence 3, Application US/09330330
; Patent No. 6274709
; GENERAL INFORMATION:
APPLICANT: Yano, Masahiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              y Match 3.4%;
Local Similarity 46.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10322 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Iwamoto, Masao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 423; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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STRANDEDNESS: sing
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                                                                                                                                                                                                                       RESULT 2
US-09-330-330-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCTTGCAACTAAACAGGTGTC----AGAATGGGAGAAATTCTATGAACACCTTCCTT 1207
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                                                                                                            1472 CTGGGCAGTTGAAAAGGCTTTTAGAAAAGAAAAGTTGCTTGATTGTTCTTAGATGATTTCT 1531
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                                                                          800 CTGAGTACCTGATAGAAGAGCTCAAGGAGAAGAGGTACTTTGTTCTTCTAGATGATCTAT
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                                      18;
Length 3925;
                                    Indels
Score 122.6; DB 3;
Pred. No. 1.7e-27;
0; Mismatches 624;
 4.0%;
                                    Conservative
                    Similarity
                                      Matches 545;
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1132 GCAATACTTACAATAGGAGCTGTGCTTGCAACTAAACAGGTGTC-----AGAATGGGAG 1185
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1802 IGTTGTGCCACTTGAAATACTTGAGTATTGGATATTCGTCATCCATATATTCACTTCCCA 1861
                                                 2492 adcitaarcacctaaaatrcctrrctracdaggatgctarcgratrgatcractgccag
                                                                                                            7027 AATCCAGAGTTGGTTAAAGAAGCAAACAAATCCTAAAGAAGTGCGATGGACTGCCCTT
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                                                                                                                                                                                                                            1922 CACTACCAAGTGAGATCAGTAAACTCCAATGTCTGCATACTCTTCGT 1968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: TRANSCO, YUICHI
APPLICANT: Sasaki, Takuji
APPLICANT: Sasaki, Takuji
APPLICANT: Wang, Zi-Xuan
APPLICANT: Wannouchi, Utako
APPLICANT: Ishimaru, Lisa
TITLE OF INVENTION: RICE GENE RESISTANT TO BLAST DISEASE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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Pred. No. 5.2e-22;
0; Mismatches 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: PasteSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/330,330
FILING DATE: 11-JUN-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 10-181455
FILING DATE: 12-JUN-1998
ATTORNEY-AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 06501/032001
TELEDOMUNICATION INFORMATION:
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STREY: 225 Franklin Street
STREY: 225 Franklin Street
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SEQ ID NO 3
LENGTH: 5.
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Patent No. 6479731
GENERAL INFORMATION:
APPLICANT: Valent, Barbara S.
APPLICANT: Bryan, Gregory
APPLICANT: Bryan, Gregory
TITLE OF INVENTION: A Pi-ta GENE CONFERRING DISEASE RESISTANCE TO PLANTS
FILE REFERENCE: BB-1136
CURRENT APPLICATION NUMBER: US/09/336,946B
CURRENT FILING DATE: 1999-06-21
PRIOR APPLICATION NUMBER: 60/095229
PRIOR APPLICATION NUMBER: 60/095229
PRIOR PILING DATE: 1998-08-04
NUMBER OF SEQ ID NOS: 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAATTCTATGAACACCTTCCTTCAGAACTAGAAATAAACCCAAGCCTGGAAGCTTTGAGG
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Sequence 68, Application US/09336946B

Sequence 68, Application US/09336946B

Patent No. 6479731

GENERAL INFORMATION:

APPLICANT: Valent, Barbara S.

APPLICANT: Bryan, Gregory

APPLICANT: E. I. du Pont de Nemours and Company

APPLICANT: B. I. du Pont de Nemours and Company

APPLICANT: B. I. du Pont de Nemours and Company

TITLE OF INVENTION: A PI-ta GENE CONFERRING DISEASE RESISTANCE TO PLANTS

FILER REFERENCE: BB-1136

CURRENT APPLICATION NUMBER: US/09/336,946B

CURRENT APPLICATION NUMBER: 60/095229

PRIOR FILING DATE: 1998-06-04

NUMBER OF SEQ ID NOS: 74

SOFTWARE: Microsoft Office 97

SEQ ID NO 68

LENGTH: 5222
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                                                                                                                                                                                      2.6%; Score 81.6; DB 4;
46.7%; Pred. No. 3.1e-14;
tive 0; Mismatches 339;
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Matches 307; Conservative
                               TYPE: DNA
; ORGANISM: Oryza sativa
US-09-336-946B-3
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; ORGANISM: Oryza sativa
US-09-993-170-57
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Sequence 57, Application US/09993170

Patent No. 6743969

GENERAL INFORMATION:
APPLICANT: Bryan, Gregory
TITLE OF INVENTION: Modification of a Plant Disease Resistance Gene
TITLE OF INVENTION: Specificity and Method for Engineering Altered
TITLE OF INVENTION: Specificity and Method for Engineering Altered
TITLE OF INVENTION: Specificity
FILE REPERENCE: BB1385 US NA
CURRENT PAPLICATION NUMBER: US/09/993,170

CURRENT FILING DATE: 2001-11-4

PRIOR FILING DATE: 2001-11-4

NUMBER OF SEQ ID NOS: 60

SOFTWARE: Microsoft Office 97

SET DATE: 5222

TYPE: DNA
                                                                                                                                           908 ACAATAAGAAGGGCAGTCGAATAGTAATAACCACTCGGAATGTTGATCTTGCGGAGAAGT
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                                                                                                       Gaps
                                                                                                       12;
                                                                   Length 5222;
                                                                    Query Match 2.6%; Score 81.6; DB 4; Length 52 Best Local Similarity 46.7%; Pred. No. 3.2e-14; Matches 307; Conservative 0; Mismatches 339; Indels
 ; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-336-946B-68
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; Sequence 60, Application US/0993170
; Patent No. 6743969
; GRENEAL INFORMATION:
   APPLICANT: Valent, Barbara
; APPLICANT: Valent, Gregory
; TITLE OF INVENTION: Modification of a Plant Disease Resistance Gene
; TILLE OF INVENTION: Specificity and Method for Engineering Altered
; TILLE OF INVENTION: Specificity and Method for Engineering Altered
; TILLE OF INVENTION: Specificity
; FILE REFERENCE 1891385 US NA
; CURRENT APPLICATION NUMBER: US/09/993,170
; CURRENT FILING DATE: 2000-11-26
; PRIOR APPLICATION NUMBER: 60/248,335
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                    GTGCCACAGCCTCACTGGTGTACCACCTTGATTTCTTGCAGATGAACGATGCCATAACAT
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                                                                                                                                              908 ACAATAAGAAGGGCAGTCGAATAGTAATAACCACTCGGAATGTTGATCTTGCGGAGAGT
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                                                                        Gaps
                                                                     12;
Length 5222;
   Score 81.6; DB 4; Length 5 Pred. No. 3.2e-14; 0; Mismatches 339; Indels
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ORGANISM: Artificial Sequence
   Query Match 2.6%;
Best Local Similarity 46.7%;
Matches 307; Conservative
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US-09-993-170-60
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LENGTH: 5696
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US-09-336-946B-1
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Sequence 1, Application US/09336946B

Patent No. 6479731

GENERAL INFORMATION:

APPLICANT: Baryan, Gregory

APPLICANT: Baryan, Gregory

APPLICANT: Bryan, Gregory

TILE OF INVENTION: A Pi-ta GENE CONFERRING DISEASE RESISTANCE TO PLANTS

FILE REFERENCE: BB-1136

CURRENT APPLICATION NUMBER: US/09/336,946B

CURRENT FILING DATE: 1999-06-21

PRIOR APPLICATION NUMBER: 06/095229

PRIOR FILING DATE: 1998-08-04

NUMBER OF FILING DATE: 1998-08-04

NUMBER OF SEQ ID NOS: 74

SEQ ID NO:

SEQ I
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     ; FEATURE:
.. OTHER INFORMATION: Description of Artificial Sequence:Chimeric
US-09-993-170-60
                                                                                                                 Length 5696;
                                                                                                         2.6%; Score 81.6; DB 4; Length 5.46.7%; Pred. No. 3.4e-14; Live 0; Mismatches 339; Indels
                                                                                                                                                                   Matches 307; Conservative
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ORGANISM: Oryza sativa
                                                                                                                                      Similarity
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                                                                                                              Query Match
                                                                                                                                            Best Local
FEATURE:
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3791 GCTGTGGATATAACTCAGAGCACATTATTAAGATTGATCCACTGGGTGATGATGTCTCAA 3850
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for Engineering Altered
                                                                     12;
Length 5757;
2.6%; Score 81.6; DB 4; Length 57;
46.7%; Pred. No. 3.4e-14;
iive 0; Mismatches 339; Indels
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Patent No. 6743969

GENERAL INPORMATION:
APPLICANT: Walent, Gregory
TITLE OF INVENTION: Modification of a Plant Dis
TITLE OF INVENTION: Specificity and Method for;
TITLE OF INVENTION: Specificity
TITLE OF INVENTION: Specificity
FILE REFERENCE: BB1385 US NA
CURRENT APPLICATION NUMBER: US/09/993,170
CURRENT PILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 60/248,335
PRIOR RILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 60

SOFTWARE: Microsoft Office 97

LENGTH: 5757
                                  Best_Local Similarity 46.7
Matches 307; Conservative
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; ORGANISM: Oryza Bativa
US-09-993-170-56
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Length 2718;

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3731 ATAATAATAGTTGCAGTAGAATACTAATAACAACAGAAATTGAACCTGTAGCTTTGGCAT 3790
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                                                                                   908 ACAATAAGAAGGGCAGTCGAATAGTAATAACCACTCGGAATGTTGATCTTGCGGAGAAGT 967
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                                           12;
    Length 5757;
2.6%; Score 81.6; DB 4; Length 5 46.7%; Pred. No. 3.4e-14; tive 0; Mismatches 339; Indels
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APPLICANT: Stansawicz, et al.; TILE OF INVERTION: B62 Resistance Gene; TILE REFERENCE: 50687; CURRENT APPLICATION WUMBER: US/09/360,186; CURRENT APPLICATION WUMBER: US/09/360,186; CURRENT APPLICATION WUMBER: 60/093,957; EARLIER PILING DATE: 1998-07-23; NUMBER OF SEQ ID NOS: 9
SOUTWARE: PatentIn Ver: 2.0
SEQ ID NO 4
                                           Matches 307; Conservative
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                        Similarity
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, NAME/KEY: CDS , LOCATION: (1)..(2718) US-09-360-186-4

FEATURE:

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                                       0; Mismatches 284; Indels
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Best Local Similarity 47.2%; Pred. No. 2.3e-08;
Matches 265; Conservative 0; Mismatches 284;
Score 62.6; DB 3;
Pred. No. 2.3e-08;
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APPLICANT: Staskawicz, Brian J
APPLICANT: Danlbeck, Douglas
APPLICANT: Tai, Thomas H
TITLE OF INVENTION: B82 RESISTANCE GENE
FILE REPERENCE: 42250/234021 (5830-4A);
CURRENT APPLICATION NUMBER: US/09/864,680A;
CURRENT APPLICATION NUMBER: US/09/860,186
PRIOR FILING DATE: 1999-07-23
PRIOR FILING DATE: 1998-07-23
PRIOR FILING DATE: 1998-07-23
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3:1
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2.0%;
                     Best Local Similarity 47.2
Matches 265; Conservative
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US-09-864-680A-4
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US-09-864-680A-4
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   Query Match
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881 GGATAAATGAAATTGCATTTCCTAAGAACAATAAGAAGGGCCAGTCGAATAGTAATAACCA 940
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ilarity 47.2%; Pred. No. 2.6e-08;
Conservative 0; Mismatches 284;
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Parent No. 6762285
GENERAL INFORMATION:
APPLICANT: Starkawicz, Brian J
APPLICANT: Dahlbeck, Douglas
APPLICANT: Tai, Thomas H
ITLE PERERENCE: 42250/234021 (5830-4A)
CURRENT APPLICATION NUMBER: US/09/864,680A
CURRENT FILING DATE: 1999-07-23
PRIOR FILING DATE: 1999-07-23
PRIOR FILING DATE: 1999-07-23
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SOFTWARE: PatentIn version 3.1
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OTHER INFORMATION:
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Best Local Simil
Matches 265; C
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US-09-864-680A-2
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US-09-864-680A-2
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  TCAAGGAGAAGAGGTACTTTGTTGTTCTAGATGATCTATGGATTTTACATGATTGGAATT
                                           755 TAAAGAGAAAGAGGTACTTAATTGTCTTGGATGATATCTGGAGTTGTGAAGTGTGGGATG
                                                                                    GGATAAATGAAATTGCATTTCCTAAGAACAATAAGAAGGGCAGTCGAATAGTAATAACCA
                                                                                                                                                                   CTCGGAATGTTGATCTTGCGGAGAGTGTGCCACAGCCTCACTGGTGTACCACCTTGATT
                                                                                                                                                                                                            872 CCCGTAATGATGAAGTAGCTTGTTATGCTGTGTAGAGAATTTTTCTTTGCGGATGAGCT
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APPLICANT: Staskawicz, et al.
TITLE OF INVENTION: B82 Resistance Gene
FILE REFERENCE: 50687
CURRENT APPLICATION NUMBER: US/09/360,186
CURRENT FILING DATE: 1999-07-23
BARLIER FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN VOWEY: 2.0
SOFTWARE: PATENTIN VOWEY: 2.0
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; NAME/KEY: CDS
; LOCATION: (93)..(2810)
US-09-360-186-2
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US-09-360-186-2
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patent No. 676288

GENERAL INFORMATION:
APPLICANT: Stackawicz, Brian J
APPLICANT: Daubleck, Douglas
APPLICANT: Tai, Thomas H
TITLE OF INVENTION: B2 RESISTANCE GENE
FILE REPERENCE: 4226/234021 (5830-4A)
CURRENT APPLICATION NUMBER: US/09/864,680A
CURRENT FILING DATE: 2001-05-24
PRIOR FILING DATE: 1999-07-23
PRIOR FILING DATE: 1999-07-23
PRIOR FILING DATE: 1999-07-23
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
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      964 CCCGTAATGATGAAGTAGCTTGTTATGCTGGTGTAGAGAATTTTTCTTTGCGGATGAGCT
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Pred. No. 1.8e-07;
0; Mismatches 284; Indels 12;
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| Patent No. 6262343
| GENERAL INFORMATION:
| APPLICANT: Staskawicz, et al.
| TITLE OF INVENTION: BS2 Resistance Gene
| FILE REFERENCE: 50687
| CURRENT APPLICATION NUMBER: US/09/360,186
| CURRENT FILING DATE: 1999-07-23
| EARLIER APPLICATION NUMBER: 60/093,957
| FARLIER FILING DATE: 1998-07-23
| NUMBER OF SEQ ID NOS: 9
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Best Local Similarity 47.2%;
Matches 265; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 1
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US-09-360-186-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ratent No. 6114605
) GENERAL INFORMATION:
) GENERAL INFORMATION:
) APPLICANT: Williamson, Valerie M. APPLICANT: Yaghoshian, Isgouhi
) APPLICANT: Yaghoshi, Jafar
) APPLICANT: Milligan, Stephen
) TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Pest Resistance in Plants
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/947,823
FILING DATE: 09-OCT-1997
CLASSITCATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/18802
FILING DATE: 09-OCT-1997
PRIOR APPLICATION NUMBER: US 60/028,191
PILING DATE: 09-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bactian, Kevin L.
REGISTRATION NUMBER: 34,774
REFIRENCE/DOCKET NUMBER: 023070-070210US
TELECOMMUNICATION INFORMATION:
TELEFRAX: (415) 576-0300
INFORMATION FOR EQUIPO:
SEQUENCE CHARACTEISTICS:
LENGTH: 3997 base pairs
TYPE: nucleic acid
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-947-823-2
Sequence 2, Application US/08947823
; Patent No. 6114605
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 85..3852
; OTHER INFORMATION: /note= "Copy 1 cDNA for M1 nematode
; OTHER INFORMATION: resistance gene of tomato"
US-08-947-823-2
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sequence 84, Appl Sequence 1016, A Sequence 1778, Appl Sequence 5, Appl Sequence 96, Appl Sequence 97, Appl Sequence 97, Appl Sequence 97, Appl Sequence 97, Appl Sequence 14, Appl Sequence 1204, Appl Sequence 35, Appl Sequence 34, Appl Sequence 33, Appl Sequence 34, Appl Sequence 33, Appl Sequence 34, Appl Sequence 3

Sequence 75977, A Sequence 31426, A Sequence 34053, A Sequence 16135, A

Seguence Sequence

Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Minimum DB Maximum DB

Database

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GCCTCCGCTGCTGCCGACGACGACCAGCCTCCTGCTGGGCGTCGAGAAAAAACATCTGGTAT
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US-10-656-394A-7

Sequence 7, Application US/10656394A

Publication No. US20040210957A1

GENERAL INFORMATION:

APPLICANT: Wang et al.

TITLE OF INVENTION: Cloning and Characterization of the

TITLE OF INVENTION: Droad-spectrum resistance gene Pi2

FILE REFERENCE: 035718/252062

CURRENT APPLICAND NUBER: US/10/656,394A

CURRENT FILING DATE: 2003-09-05

NUMBER OF SEQ ID NOS: 16

SEQ ID NO 7

LENGTH: 3099
7 US-10-352-179-90

10 US-10-352-179-84

8 US-10-437-963-41016

8 US-10-437-963-49433

10 US-10-437-963-49433

10 US-10-437-963-49433

10 US-10-437-963-49403

10 US-10-437-963-4940

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 3099; Conservative 0; Mismatches
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   TYPE: DNA
ORGANISM: Oryza minuta
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; NAME/KEY: CDS
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Sequence 13, Appl
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Sequence 92, Appl
Sequence 93, Appl
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                                                                                                                   February 13, 2005, 07:09:17; Search time 1092.99 Seconds (without alignments) 16729.796 Million cell updates/sec
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Publication No. US20040210957A1;
GENERAL INFORMATION:
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CURRENT APPLICATION UNMER: US/10/656,394A
CURRENT FILING DATE: 2003-09-05;
NUMBER OF SEQ ID NOS: 16;
SOFTWARE: FeatSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 99090
TTME: DNA
TTME: DNA
GRGANISM: OFYZE minuta
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Best Local Similarity 99.9%;
Matches 2954; Conservative
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; LOCATION: 23216
; OTHER INFORMATION: n =
US-10-656-394A-13
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19673   MACHANIAGAN RECONSTRUCTION	RESULT 3 US-10-552-179-88 JOSEPH SEQUENCE 88. Application US/10352179 JOSEPH SEQUENCE 88. Application No. US20040006788A1 JOSEPH SEQUENCE WAS GOO-liang JOSEPH SEQUENCE APPLICANT: Wang GOO-liang JOSEPH SEQUENCE SEQUENCE SEQUENCE APPLICANT: Liu, Guifu JOSEPH SEQUENCE SECONDARY OF THE REFERENCE: 22727/04108
1016   MANTATICOLAMAGNEGITCHANCIANTEGRATICATION TO   1016   MANTATICOLAMAGNEGITCHAN TAKEN TO   1016   MANTATICOLAMAGNEGITCHAN TAKEN THE   1115   MANTATICOLAMAGNEGITCHAN TAKEN TAKEN THE   1115   MANTATICOLAMAGNEGITCHAN TAKEN TAKEN THE   1115   MANTATICOLAMAGNEGITCHAN TAKEN TAKEN TAKEN THE   1115   MANTATICOLAMAGNEGITCHAN TAKEN	2036 TATGCCTGCCTAAAGTATTCACACCTTTAGTTAGTCGCGATGATCGTGCAAAACAAATTG 2095

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CURRENT APPLICATION NUMBER: US/10/352,179
CURRENT FILING DATE: 2003-01-27
PRIOR APPLICATION NUMBER: 60/352,106
PRIOR PILING DATE: 2002-01-25
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn version 3.1
SOFTWARE: PatentIn version 3.1
SEQ ID NO 88
TYPE: DNA
ORGANISM: Oryza minuta
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Best Local Similarity 96.8
Matches 2975; Conservative
                                                                                                                                  FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(3096)

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              GAAGTGAGTAGCAGGAACACACGCTACAGTTTAGTCAAGCCTATTTCCTCTGGCACAGAG
                                              GAAGTGAGTAGCAGGAACACACGCTACAATTTAGTCGAGCCTATTTCCTCCGGCACAGAG
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Publication No. US20040210957A1

GENERAL INFORMATION:

TITLE OF INVENTION:

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                    GGTATATCAAAGATGAGCTAAAAACGATGCAAGCATTCCTTAGAGCTGCTGAACTTATGA
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Publication No. US200400678BA1
APPLICANT: Usu, Guifu
APPLICANT: Liu, Guifu
APPLICANT: Liu, Guifu
APPLICANT: Liu, Guifu
APPLICANT: Liu, Guifu
CURRENT PLING DATE: 22727/04108
CURRENT PLING DATE: 2003-01-27
PRIOR APPLICATION NUMBER: 60/352,106
PRIOR APPLICATION NUMBER: 60/352,106
PRIOR APPLICATION NUMBER: 60/352,106
PRIOR APPLICATION NUMBER: 2002-01-25
NUMBER OF SEQ ID NOS: 97
SOFTWARE: Patentin version 3.1
SEQ ID NO 83
LENGTH: 76272
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_41056C.1
US-10-437-963-37316
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Pred. No. 0;
0; Mismatches
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILLING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 37316
LENGTH: 4596
TYPE: DNA
ORGANISM: Oryza sativa
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Best Local Similarity 98.3%;
Matches 2604; Conservative
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                                                                    CTCTTTCGAGGAAGATCTTTGAAAGCGAAGAAGACATTAGGAAGAACTTCCCTTGCAATG
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                                        CTAATGATGGTCCCGGCCAAGGTAATCTGTGTTGGCGATGGGTGGTTTAGGCAAGACAG
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 Pred. No. 0;
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Best Local Similarity 96.1%;
Matches 2453; Conservative
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                       GCAGCTCACCCCTGTTGGAAAGATAGAATAGGCGAGTGCCAGGTTGGAATCTGGGATTA 2758
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; Publication No. US20040210957A1
; GENERAL INFORMATION:
; APPLICANT: Wang et al.
; TITLE OF INVENTION: Droad-spectrum resistance gene Pi2; TITLE OF INVENTION: Droad-spectrum resistance gene Pi2; FILE REFERENCE: 035718/525062
; CURRENT APPLICATION NUMBER: US/10/656,394A
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2997
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGAATGATAG 3068
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ORGANISM: Oryza minuta
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; LOCATION: (1)
US-10-656-394A-11
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Sequence 2483, Application US/10437963
; Sequence 2483, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: A Rosa, Thomas J.
; APPLICANT: Abou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Wu, Wei
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules
; TITLE REPERENCE: 38-21(5321)B
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 2483
; LENGTH: 2982
; TENGTH: 2982
                                                                                                                                                                                                                                                                                  2882 ACAGTGACCGAAGGTATCACGACCTGGGGGCTGAAGCCGAAGGATCTTCTATAGAAGTGC 2941
                                                                               2417 TIAGAACACTITCGATTIACGATTIGGATCAGCTAAGAGAGATTAGATITGAGGACGGCA
                                                                                                                                    GCTCGCCCCAGTTGGAAAAGATAGAAATCAGATTCTGCAGGTTGGAATCAGGGATTATTG
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US-10-437-963-2483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 60.7%; Score 1882; DB 18;
Best Local Similarity 78.9%; Pred. No. 0;
Matches 2352; Conservative 0; Mismatches 445;
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ORGANISM: Oryza sativa
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ACCGAAGTATGATTCAACGATCAAGAGTGGGCATAGCAGGAAAAATTAAGACTTGTCGAA 1276
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                       GTGACAGACCCAAGAGTCTAGCACTGCAGTTTGTCCAGATCAATTGAGGATGTTACGGG
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                                                  CACTCGCCACATAGCATTCCATGGGAGTATGTCCTGCAAAACTGGATTGGATTGGAGCAT
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TCCCTGCAATCTCCGTGTGGATGCTGAGGGGTCCTCAGGAAATGGAACACTTAAATGT
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Publication No. US20040210957A1

GRENEAL INFORMATION:

TITLE OF INVENTION: Cloning and Characterization of the

TITLE OF INVENTION: Droad-spectrum resistance gene Pi2;

FILE REFERENCE: 035718/222062

CURRENT APPLICATION NUMBER: US/10/656,394A

CURRENT FILING DATE: 2003-09-05

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 15

LENGTH: 2422

TYPE: DNA

ORGANISM: Oryza minuta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: misc_feature
; LOCATION: 2014, 2043, 2099, 2114, 2154, 2172,
; LOCATION: 2268, 2299, 2333, 2337, 2339, 2356
; OTHER INFORMATION: n = A,T,C or G
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RESULT 13

US-10-352-179-84

i Sequence 84, Application US/10352179

publication No. US2004006788A1

GENERAL INFORMATION:

APPLICANT: Mang, Guo-liang

APPLICANT: Liu, Guifu

TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pl
FILE REFERENCE: 22727/04108

CURRENT APPLICATION NUMBER: US/10/352,179

PRIOR APPLICATION NUMBER: 60/352,106

PRIOR PLILNG DATE: 2002-01-25

NUMBER OF SEQ ID NOS: 97

SOFTWARE: PatentIn version 3.1

SEQ ID NO 84

LENGTH: 2940
                                          CCAACCTCATGGTCCTTTATCTTCATTCCAATGCTTACCATGGGGGAGAAGCTAGTATTCA
                                                                                                                                                                                                                                            GATACGGAAGTAAAGTGGCTAGGCTTGGTCAGCTGGAGGAGAAGTGCGCACACACCCAA
            2319 TCCAGAAGCTCTGTTTCCTACAATCTCTCCATGTGAATGCTGTGGGATTTTCAGGTATTG
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Pred. No. 0;
0; Mismatches
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ORGANISM: Oryza minuta
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; LOCATION: (1)..(2940)
; OTHER INFORMATION:
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 ; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
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US-10-437-963-41016
                                                                        DB 18;
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; Publication No. US20040123343A1
; GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERRICE: 38-21(53221)
CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT APPLICATION NUMBER: US/10/437,963
; SEQ ID NO 41016
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Oy 2037 AIGCCTGCCTAAAGTAITCACACCTITAGITA	Qy 2097 TGAATTGCACATGGCCACCAAAGTTGCTGGT	2157	2217	2277	Oy 2337 CCTCCAATCTCTCCTGTGGACTCTCTCGGAAA  Db 2343 TCTGCAATCTCTCCGTGTGGATGCTGAAGAAT  2363 ACAMTACTATATATATATATATATATATATATATATATAT	2403	2463	2517		2643	2703	2757 2763	2817 2823 2823	Db 2883 AATGGCAGAGGATCGAAGTCATCATGACCTAG	RESULT 15 US-10-656-394A-1 ; Sequence 1, Application US/10656394A : publication No. US2004021095781		FILE REFERENCE: 035718/252062 ; CURRENT APPLICATION NUMBER: US/10/656,394A ; CURRENT FILING DATE: 2003-09-05 ; NUMBER OF SEQ ID NOS: 16
960 GGAGAAGTGTGCCACAGCCTCACTGGTGCACCTTGATTTCTTGCAGATGAACGATGC 1019 	107	CGAATTGTAAATAAATGTGGTCTACCACCGCTGGCATACT	1140 TACAATAGGAGCTGTGCTTGCAACTAAACAGGTGTCGAATGGGAGAATTCTATGAACA 1199 	1200 CCTTCCTTCAGAACTAGAAATAAACCCAAGCCTGGAAGCTTTGAGGAGAATGGTGACCCT 1259 	1260 AGGTTACAACCACCTACCATTTGAAACCATGCTTTTTGTATCTAAGTATCTTTCC 1319 	1320 TGAGGATTTTGAAATCAAAGGAATCGTCTAGTAGGTAGATGGATAGCAGAAGGGTTTGT 1379 	1380 TAGACCAAAGGTTGGGATGACGACTAAGGATGTCGGAGAAGTTACTTTAATGAGCTAAT 1439 	1440 CAACCGAAGTATGATTCAACGATCAAGAGTGGGCATAGCAGGAAAAATTAAGACTTGTGG 1499 	1500 AATTCATGATATCATCGTGATATCACAGTTTCAATCTCGAGACAGGAAAATTTTGTATT 1559 	1560 ATTACCAATGGGAGATGGCTCTGATTTAGTTCAGGAAAACACTGGCCACATAGCATTCCA 1619 	1620 TGGGAGTATGTCCTGCAAAACTGGATTGGATTGGAGCATTATTCGATCATTAGCTAFTTT 1679 	1680 TGGTGACAGACCCAAGAGTCTAGCACATGCAGTTTGTCCAGATCAATTGAGGATGTTACG 1739 	1740 GGTCTTGGATCTTGAAGATGTGACATTCTTAATCACTCAAAAAGATTTCGACCGTATTGC 1799 	1800 ATHGITGRGCCACTIGAATACTHGAGTATTGGATATTGGTCATCCATATATTCACTTCC 1859 1803 GITGITGGGCCACATGAAATATTTGCAAGAGCCTCAACTATTATACACTTCC 1862	1860 CAGATCCATTGGTAAACTACAGGGCCTACAAACTTTGAACATGCCGAGCACATACAT	1920 AGCACTACCAAGTGAGATCAGTAAACTCCAATGTCTGCATACTTCGTTGTATAGGACA 1979 	1980 GTTTCATTATGACAACTTTAGTCTAAACCACCCAATGAAGTGCATAACTAACACAAT 2036 
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Best Local Similarity 71.5%;
Matches 2085; Conservative
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FRATURE:
NAME/KEY:
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SOFTWARE: FastSEQ
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GITTCAITATGACAACTITAGTCTAAACCACCCAATGAAGTGCAIAACTAACACAT 2 	AIGCTIGCCIAAAGIAITGACACCITTAGITAGICGGAIGAICGIGGAAAAGAAAITIGC 2 	TGRATTGCACATGGCCACCAAAAGTTGCTGGTCTGAATCAATC	aggaataggtaagttgcgagacttgcaggttctagagtatgtagatatcagggggccgg 2 	Tagtagagcaatcaaagagctggggcagttaagcaagctgaggaattaggtgtgacaac 2 	AAACGGGTCGACAAAGGAAAAATGTAAGATACTTTATGCAGCCATTGAGAAGCTCTCTTC 2 	CCTCCAATCTCTCCATGTGGATGCTGCAGAATCTCAGATGGTGGAACACTTGAGTGCCT 2	AGATTCTATTTCATCTCCTCCTCCTCTCTGAGGACACTCGTGTTGGATGGA	GGAGATGCCTAACTGGATTGAGCAGCTCACTCACCTGAAGAAGATCTACTTATTGAGGAG 2 	CAAACTAAAGGAAGGTAAAACCATGCTGATACTTGGGGCACTGCCCAACCTCATGGTCCT 2	TCATCTTTATCGGAATGCTTACCTTGGGGAGAAGCTAGTATTCAAAACAGGAGATTCCC 2	aaricttagaacactttggatttatgaattggatcagctaagagagag	CGGCAGCTCACCCCTGTTGGAAAAGATAGAAATAGGCGAGTGCAGGTTGGAATCTGGGAT 2 	TACTGGTATCATTCACCTTCCAAGGTCTCAGGAGATTCCAATTAGATACGGAAGTAAGT	GGCTGGGCTTGGTCAGCTGGAGGGAGAGTGAACGCACACACA	AATGTACAGTGACCGAAGGTATCACGACCTGGGGG 2911 	
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Search completed: February 13, 2005, 20:04:19 Job time : 1102.99 secs

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Matches 1032; Conservative 0; Mismatches
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Adf17765 Solanum b	ADF17765 AC	7	970	13.1	989	45
dh51546 Plant inf		0	945	13.1	692.5	44
Aay44818 Potato Gp		m	912	13.3	701.5	43
		m	938	13.3	703	42
Aau02147 Rx 193, m		4	937	13.5	713	41
	ADI45353 AC	8	1471	13.6	717.5	40
		4	937	13.7	722	39
Aau02146 Rx 39, mo		4	937	13.7	722	38
	_	4	937	13.8	727	37
au02145 Rx 72, mo	ın	4	937	13.8	727	36
Aay52152 Potato re		7	937	13.8	729	35
RX 32,	0	4	937	13.9	731	34
		4	937	13.9	734	33
Adc08012 Rice prot	ADC08012 Ac	۲	2827	15.5	815.5	32
	ABB06872 AB	4	922	15.5	818	31
Abb06873 Barley Ml	ABB06873 Al	4	945	15.6	823.5	30
	ABB06879 Al	4	939	16.0	842.5	53
	ABB06874 AB	4	926	16.4	862.5	28
Abb06878 Rghla pro	ABB06878 AB	4	967	16.6	873	27
	ABBURG / /	4	,		0.00	9

## ALIGNMENTS

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The invention relates to novel broad-spectrum resistance gene Pi2 and the NSS(1-6) genes present in the Pi2 gene cluster region. The rice Pi2-like disease resistance nucleic acid molecules are useful for enhancing disease resistance in plants. The present sequence represents a rice NBS4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New rice Pi2-like disease resistance nucleic acid molecule that confers disease resistance in plants, useful for creating or enhancing disease
                                                                                                                                                                                                                                  Pi2; NBS4; plant protectant; gene therapy; rice; disease resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 8; 120pp; English.
  protein, 1032 AA
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18-MAR-2003; 2003US-0455713P.
05-SEP-2003; 2003US-00656394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-SEP-2003; 2003WO-US027913.
                                                                                                                                                                      O. minuta NBS4 polypeptide
                                                                                                                 (first entry)
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ADM72245 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUSSRNTRYSLVKPISSGTEIDMDSYAEDIRNQSARNVDEAELVGFSDSKKRLLEMIDTN 180
                                                                                                                                                               ANDGPAKVICVVGMGGLGKTALSRKIFESEEDIRKNPPCNAWITVSQSFHRIELLKDMIR 240
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                                                 KDELLKVWAEQIRDLSYDIEDSLDEFKVHIESQTLFRQLVKLRERHRIAIRIHNLKSRVE 120
                                                                                                 EVSSRNTRYSLVKPISSGTEIDMDSYAEDIRNOSARNVDEAELVGFSDSKKRLLEMIDTN 180
                                                                                                                                                                                                                     QLLGPSSLDQLLQELQGKVVVQVHHLSEYLIEELKEKRYFVVLDDLWILHDWNWINEIAF 300
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               QLLGPSSLDQLLQBLQGKVVVQVHILSEYLIEELKEKRYFVVLDDLWILHDWNWINEIAF
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                                                                                                                                                ANDGPAKVI CVVGMGGLGKTALSRKI FESEEDIRKNFPCNAWI TVSQSFHRIELLKDMIR
                                                                                                                                                                                                                                                                                                                                            GYNHLPSHLKPCFLYLSIPPEDFEIKRNRLVGRWIAEGFVRPKVGMTTKDVGESYFNELI
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  MAETVLSMARSLVGSAISKAASAADETSLLLGVEKDIWYIKDELKTMQAFLRAAELMKK
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The invention comprises the amino acid and coding sequences of nucleotide binding site (NBS) proteins from the Oryza minuta P19 locus (bacterial blight and rice blast resistance genes). The DNA sequences may be used as markers for resistance to infection with Magnaporthe grisea in plant breeding programs. The present amino acid sequence represents an NBS protein encoded by a gene from the Oryza minuta Pi9 locus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2 and NBS3, useful for producing plants resistant to Magnaporthe grisea infection.
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                                                                                    nucleotide binding site; NBS; Pi9 gene; bacterial blight; rice blast;
plant breeding; transgenic plant; plant.
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                                            protein #5
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                                            Oryza minuta Pi9 locus nucleotide binding site (NBS)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 93; 136pp; English
                                                                                                                                                                                                                                                                                                                                       25-JAN-2002; 2002US-0352106P
01-FEB-2002; 2002US-0353304P
                                                                                                                                                                                                                                                                                             27-JAN-2003; 2003US-00352179
(first entry
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N-PSDB; ADI57175.
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                                                                                                                                                                                                                                                                                                                                                                                                         (WANG/) WANG G. (LIUG/) LIU G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu G;
                                                                                                                                                          Oryza minuta
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LLGPSSLDQLLQELQGKVVVQVHHLSEYLIEELKEKRYFVVLDDLWILHDWNWINEIAFP 301

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The invention comprises the amino acid and coding sequences of nucleotic binding site (NBS) proteins from the Oryza minuta Pi9 locus (bacterial blight and rice blast resistance genes). The DNA sequences may be used a markers for resistance to infection with Magnaporthe grises in plant breeding programs. The present amino acid sequence represents an NBS protein encoded by a gene from the Oryza minuta Pi9 locus.
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95.5%; Pred. No. 0;
tive 14; Mismatches
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                                                           25-JAN-2002; 2002US-0352106P.
01-FEB-2002; 2002US-0353304P.
                                 27-JAN-2003; 2003US-00352179
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Matches 976; Conservative
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                                                                                                      WANG G.
LIU G.
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    08-JAN-2004
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QKMVERIVNKCGRLPLAILTIGAVLATKHVEWEKFYEQLPSELEINPSLEALRRMYTLG 480
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                                              KNNKKGSRIVITTRNVDLAEKCATASLVYHLDFLQMNDAITLLLRKTNKNHEDMESNKNM 361
                                                                                                                                                                                                                                         SMSCKTGLDWSIIRSLAIFGDRFKSLAHAVCLDQLRMLRVLDLEDVTFLITQKDFDRIAL
                                                                                                      QKWVERIVNKCGRLPLAILTIGAVLATKQVSEWEKFYEHLPSELEINPSLEALRRMVTLG
                                                                                                                                                               YNHLPSHLKPCFLYLSIFPEDFEIKRNRLVGRWIABGFVRPKVGMTTKDVGESYFNELIN
                                                                                                                                                                                                                           RSMIQRSRVGIAGKIKTCRIHDIIRDITVSISRQENFVLLPMGDGSDLVQENTRHIAFHG
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plant.
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nucleic acid molecules are useful for enhancing in plants. The present sequence represents a rice NBS2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New rice Pi2-like disease resistance nucleic acid molecule that confers
disease resistance in plants, useful for creating or enhancing disease
                                                                                                                                                                                                                                                                                LKEGKTMLILGALPNLMVLHLYRNAYLGEKLVFKTGAFPNLRTLMIYELDQLREIRFEDG
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                                     FVYDNPSLNHPMKCITNTICLPKVFTPLVSRDDRAKQIAELHMATKSCWSESFGVKVPKG
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2003US-0455713P.
2003US-00656394.
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                                AFPKNNKKGSQIVITTWNVDLAEKCATASLVYHLDFLQMNDAITLLLRKTNKNHEDMESN
                                                                                                                                                                                                                                           LINRSMIQRSRVGIAGKIKTCRIHDIIRDIIVSISRQENFVLLPMGDGSDLVQENTRHIA
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TNANDGPAKVICVVGMGGLGKTALSRKIFESEEDIRKNFPCNAWITVSQSFHRIELLKDM
                                                                                                      AFPKNNKKGSRIVITTRNVDLAEKCATASLVYHLDFLQMNDAITLLLRKTNKNHBDMESN
                                                                                                                                                                                               KNMQKAVERIVNKCGRLPLAILTIGAVLATKQVSEWEKFYEHLPSELEINPSLEALRRMV
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                                                                                                                                                                                                                                                                                                                   LINRSMIQRSRVGIAGKIKTCRIHDIIRDITVSISRQENFVLLPMGDGSDLVQENTRHIA
                                                                                                                                                                                                                                                                                                                                                                                      PHGSMSCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLBDVTFLITQKDFDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protectant; gene therapy; rice; disease resistance.
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    minuta NBS1 polypeptide

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              YSDRRYHDLGAEAEGSSIEVQTADPVPDAEGSVTVAVEATDPLPEQEGESSQSQVITLTT 1020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KDELLKVWAEQIRDLSYDIEDSLDEFKVHIESQTLFRQLVKLRERHRIAIRIHNLKSRVE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New rice P12-like disease resistance nucleic acid molecule that confers
disease resistance in plants, useful for creating or enhancing disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAETVLSMARSLVGSAISKAASAAADETSLLLGVEKDIWYIKDELKTMQAFLRAAELMKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pi2; NBS6; plant protectant; gene therapy; rice; disease resistance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 8; Length 998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.4%; Score 4237; DB 8; Length 9
84.2%; Pred. No. 0;
ive 17; Mismatches 47; Indels
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                                                                                                                                                                                                          ADM72249 standard; protein; 998
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18-MAR-2003; 2003US-0455713P.
05-SEP-2003; 2003US-00656394.
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                                                                                    NDSEEIGTAQAG 1032
                                                                                                        minuta NBS6 polypeptide
                                                                                                                                                                                                                                                                              (first entry)
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Matches 854; Conservative
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The invention comprises the amino acid and coding sequences of nucleotide binding site (NBS) proteins from the Oryza minuta Pi9 locus (bacterial blight and rice blast resistance genes). The DNA sequences may be used as markers for resistance to infection with Magnaporthe grises in plant breeding programs. The present amino acid sequence represents an NBS protein encoded by a gene from the Oryza minuta Pi9 locus.
                                                                                             779
                                                            721
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                                                                                                                                                                              KLKEGKTMLILGALPNLMVLHLYRNAYLGEKLVFKTGAFPNLRTLWIYELDQLREIRFED 899
                                                                                                                                                                                                                                                  GLKDGKTWEILGALPNIAVLRLYRNAYADEKMTFRRGTFPNLRCLDIYLLKQLREIRFEB 901
                                                                                                                                                                                                                                                                                      GSSPLLEKIEIGECRLESGITGIIHLPKLKEIPIRYGSKVAGLGQLEGEVNAHPNRPVLL 959
                                                                                                                                                                                                                                                                                                          encoding nucleotide binding site (NBS) proteins NBS1, NBS2 inl for producing plants resistant to Magnaporthe grisea
                                                 SGSGYFSIIDNPKECLMITMCLPMVFLTSINFSDRVKLIPBICMSCSTRWSDTKGVRVPR
LLRHMKYLNPARASTIYTLPRSIGKLQCLQILNMREANISALTTEVTKLQNLRSLRCSRR
                                FHYDNFS-LAHPMKCITNTICLPKVFTPLVSRDDRAKQIAELHMATKSCWSESIGVKVPK
                                                                                             GIGKLRDLQVLEYVDIRRTSSRAIKELGQLSKLRKLGVTTNGSTKEKCKILYAAIEKLSS
                                                                                                                                                          LOSLHVDAAGISDGGTLECLDSISSPPLLRTLVLDGILEEMPNWIEQLTHLKKIYLLRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleotide binding site; NBS; Pi9 gene; bacterial blight; rice blast; plant breeding; transgenic plant; plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza minuta Pi9 locus nucleotide binding site (NBS) protein #1
                                                                                                                                                                                                                                                                                                                                                      MYSDRRYHDLGAEA-----EGSSIEVQTA 983
                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 85; 136pp; English.
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01-FEB-2002; 2002US-0353304P.
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N-PSDB; ADI57167.
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and NBS3, useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NRSMIQRSRVGIAGKIKTCRIHDIIRDITVSISRQENFVLLPMGDGSDLVQENTRHIAFH 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLCHLKYLSIGYSSSIYSLPRSIGKLQGLQTLNMPSTYIAALPSEISKLQCLHTLRCIGQ 660
                                                                                                                                                                                                                                                                                                        The invention relates to novel broad-spectrum resistance gene Pi2 and the NSS(1-6) ganes present in the Pi2 gene cluster region. The rice Pi2-like disease resistance nucleic acid molecules are useful for enhancing disease resistance in plants. The present sequence represents a rice NBS1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QLLGPSSLDQLLQELQGKVVVQVHHLSEYLIEELKEKRYFVVLDDLWILHDWNWINEIAF 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New rice Pi2-like disease resistance nucleic acid molecule that confers disease resistance in plants, useful for creating or enhancing disease resistance in plants.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 993;
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                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 2; 120pp; English
                                2002US-0409216P.
2003US-0455713P.
2003US-00656394.
   38-SEP-2003; 2003WO-US027913
                                                                                               (OHIS ) UNIV OHIO STATE
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                                                                                                                                                                                N-PSDB; ADM72238
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 993 AA;
                                  09-SEP-2002;
18-MAR-2003;
                                                                05-SEP-2003;
                                                                                                                                                                                                                                                                                                                                                                        polypeptide.
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                                                                                                                           EVSSRNTRYSLVKPISS-GTEIDMDSYAEDIRNQSARNVDEAELVGFSDSKKRLLEMIDT 179
                                                                                                                                                                                                                                                      PPKNNKKGSRIVITTRNVDLAEKCATASLVYHLDFLQMNDAITLLLRKTNKNHEDMESNK 359
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                                                     ALLCHLKYLSIGYSSSIYSLPRSIGKLQGLQTLNMPSTYIAALPSBISKLQCLHTLRCIG
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                                          MAETVLSMARSLVGSAISKAASAAADETSLLLGVEKDIWYIKDELKTMQAFLRAAELMKK
                                                                                                                                                                                                                                                                                                                                        LGYNHLPSHLKPCPLYLSIPPEDFEIKRNRLVGRWIAEGFVRPKVGMTTKDVGESYFNEL
                      Gaps
                     э;
  979;
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atch
58.2%; Score 3063.5; DB 8; Length
cal Similarity 62.9%; Pred. No. 1.5e-256;
611; Conservative 141; Mismatches 217; Indels
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QMAEDRSHHDLG 971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention comprises the amino acid and coding sequences of nucleotic binding site (NBS) proteins from the Oryza minuta P19 locus (bacterial blight and rice blast resistance genes). The DNA sequences may be used markers for resistance to infection with Magnaporthe grises in plant breeding programs. The present amino acid sequence represents an NBS protein encoded by a gene from the Oryza minuta P19 locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KDELLKVWAEQIRDLSYDIEDSLDEFKYHIESQTLFROLVKLRERHRIAIRIHNLKSRVE
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                                                                                                                                                                                                                                               nucleotide binding site; NBS; Pi9 gene; bacterial blight; rice blast;
plant breeding; transgenic plant; plant.
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                                                                                                                                                                                          Oryza minuta Pi9 locus nucleotide binding site (NBS) protein #2
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48.9%; Score 2575; DB 8; Length 5
Best Local Similarity 54.9%; Pred. No. 4.9e-214;
Matches 535; Conservative 166; Mismatches 244; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encoding nucleotide binding site to for producing plants resistant
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01-FEB-2002; 2002US-0353304P.
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                                                                                                                                        (first entry)
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and NBS3, useful
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LIU G.
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                                                                                            GQFHYDNFSLNHPMKCITNTICLPKVFTPLVSRDDRAKQIAELHMATKSCWSE---SIGV 715
                                                                                                                                                                 LONSOLEEDKTMEILGELPNIMLLFLSWRA-------VLIIRNOKOLKEV 875
                                                                                      GSMSCKT-GLDWSIIRSLAIFG-DRPKSLAHAVCPDQLRMLRVLDLEDVTFLITQKDFDR 598
                                                                                                              IALLCHLKYLSIGYSSSIYSLPRSIGKLQGLQTLNMPSTYIAALPSEISKLQCLHTLRCI 658
                                                                                                                        654
                                       KVPKGIGKLRDLOVLEYVDIRRISSRAIKELGQLSKLRKLGVTINGSTKEKCKILYAAIE
                                                                                                                                                                                                                                     KLSSLQSLHVDAAGISDGGTLECLDSISSPPPLLRTLVLDGILEEMPNWIEQLTHLKKIY
                                                                                                                                                                                                         LLRSKLKEGKTMLILGALPNLMVLHLYRNAYLGEKLVFKTGAFPNLRTLWIYELDQLREI
                                                                                                                                                                                                                                RFEDGSSPLLEKIEIGECRLESGITGIIHLPKLKEIPIRYGSKVAGLGQLEGEVNAHPNR
                                                                NRSMIQRSRVGIAGKIKTCRIHDIIRDITVSISRQENFVLLPMGDGSDLVQENTRHIAFH
                 MQKMVERIVNKCGRLPLAILTIGAVLATKQVSEWEKFYEHLPSELEINPSLEALRRMVTL
                                                                                                                                                                                                                                                                                                                                       uny site; NBS; Pi9 gene; bacterial blight; rice blast;
transgenic plant; plant.
                                                                                                                                                                                                                                                                                                                                 Oryza minuta Pi9 locus nucleotide binding site (NBS) protein #4
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01-FEB-2002; 2002US-0353304P.
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                                                                                                                                                                                                                                                                                               standard; protein;
                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                      PVLLMYSDRRYHDLG
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PMLRLFGERSRHDLG
                                                                                                                                                                                                                                                                                                                     (first
                                                                                                                                                                                                                                                                                                                                            nucleotide binding
                                                                                                                                                                                                                                                                                                                                                  breeding;
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The invention comprises the amino acid and coding sequences of nucleotide binding site (NBS) proteins from the Oryza minuta Pi9 locus (bacterial blight and rice blast resistance genes). The DNA sequences may be used as markers for resistance to infection with Magnaporthe grisea in plant breeding programs. The present amino acid sequence represents an NBS protein encoded by a gene from the Oryza minuta Pi9 locus.
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EVSTRNIRYNLIENDLTCTTTDERNLFMEDIRNQ-ANNIEEADLVGFSGPKRELLDLIDV 178
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                                    Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2 and NBS3, useful for producing plants resistant to Magnaporthe grisea infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVSSRNTRYSLVK-PISSGTEIDMDSYAEDIRNQSARNVDEAELVGFSDSKKRLLEMIDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FP-KNNKKGSRIVITTRNVDLAEKCATASLVYHLDFLQMNDAITLLLRKTNKNHEDMESN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAETVLSMARSLVGSAISKAASAAADETSLLLGVEKDIWYIKDELKTMQAFLRAAELMKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                      KDELLKVWAEQIRDLSYDIEDSLDEFKVHIESQTLFRQLVKLRERHRIAIRIHNLKSRVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ROLLGPSSLDQLLQELQGKVVVQVHHLSEYLIEELKEKRYFVVLDDLWILHDWNWINEIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLGYNHLPSHLKPCFLYLSIFPEDFEIKRNRLVGRWIAEGFVRPKVGMTTKDVGESYFNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NANDGPAKVICVVGMGGLGKTALSRKIFESEEDIRKNFPCNAMITVSQSFHRIELLKDMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KOMOKAVERIVNKCGRLPLAILTIGAVLATKQVSEWEKFYEHLPSELEINPSLEALRRMV
                                                                                                                                                                                                                                                                                                                                                                                         94;
                                                                                                                                                                                                                                                                                                                                                     Length 1054;
                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                           Conservative 149; Mismatches 266;
                                                                                                                                                                                                                                                                                                                                                     44.9%; Score 2367; DB 8; 50.3%; Pred. No. 6.7e-196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIALLCHLKYLSIG-----YSSSIYSLPRS-
                                                                                                                                      Claim 1; SEQ ID NO 91; 136pp; English
2004-121064/12
                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 516; Conserv
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                    N-PSDB; ADI57173
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Mismatches 134;

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                                                                                                                                 The invention relates to novel broad-spectrum resistance gene Pi2 and the NSS(1-6) genes present in the Pi2 gene cluster region. The rice Pi2-like disease resistance nucleic acid molecules are useful for enhancing disease resistance in plants. The present sequence represents a rice NBS3
                 921
                                                                                                                                                        IIHLPKLKEIPIRYGSKVAGLGQLEGEVNAHPNRPVLLMYSDRRYHDLGAEAEGSSIEVQ 981
                                                                                                                                                                         IIHLPRLKEISLGYGSKVARLGOLEGEVRTHPNHPVLRMREDRSDHDLACDAEGSPVEVE 965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      confers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Pi2-like disease resistance nucleic acid molecule that conferi
resistance in plants, useful for creating or enhancing disease
        TKSCWSESIGVKVPKGI----GKLRDLQVLEYVDIRRTSSRAIKELGQLSKLRKLGVTTN
                                            GSTKEKCKILYAAIEKLSSLQSLHVDAAGISDGGTLECLDS------ISSPPP
                                                             GIHKGKMDTLYSYPEALPPTIS------PCECCGEFRYWNTSVYRFYFISSSP-
                                                                                LLRTLVLDGILEEMPNWIEQLTHL-KKIYLLRSKLKEGKTMLILGALPNLMVLHLYRNAY
                                                                                                                   LGEKLVFKTGAPPNLRTLWIYELDQLREIRFEDGSSPLLEKIE-IGECR----LESGITG
                                                                                                                                                                                                                                                                                                                                     plant protectant; gene therapy; rice; disease resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 660;
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Pred. No. 1.3e-174;
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                                                                                                                                                                                                                                                                                                                                                                                                                              09-SEP-2002; 2002US-0409216P.
18-MAR-2003; 2003US-0455713P.
05-SEP-2003; 2003US-00656394.
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                                                                                                                                                                                                                                                                                                                    O. minuta NBS3 polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease resistance in resistance in
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                                                                                                                                                                                                              970
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Best Local Similarity
                                                                                                                                                                                           TADPV 986
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                                                                                                                                                                                                                                                                                                                                                                                           18-MAR-2004
                                                                                                                                                                                                                                                                                                                                     Pi2; NBS3;
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                                                    QLLGPSSLDQLLQBLQGKVVVQVHHLSEYLIEELKEKRYFVVLDDLWILHDWNWINEIAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GYNHLPSHLKPCFLYLSIFPEDFEIKRNRLVGRWIAEGFVRPKVGMTTKDVGESYFNELI
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01-FEB-2002; 2002US-0353304P.
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DVSQRNVRYHLIKGSAKAT-----INSTEQSSVIATAIFGIDDARRAAKQDNQRV 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to the isolation of novel rice blast fungus (Pyricularia grises) resistance genes from rice strain BL-1. The genes are designated Pi-b (AAA11351). The genes are designated Pi-b (AAA11351). The genes can be used for creating rice which has high blast fungus resistance. This sequence represents the protein encoded by the Pi gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 NSKVVKTWVKQVRDTAYDVEDSLQDFAVHLKRPSWWRFPRTLLERHRVAKQMKELRNKVE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKCFQKCRKGSRIIVSSTQVEVASLCAGQESQASELKQLSADQTLYAFYDKGSQIIEDSV 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRDFVQSLVNQLHATQGVEALLEKEKTEQDLAKKFNGCVNDRKCLIVLNDLSTIEEWDQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 KDELLKVWAEQIRDLSYDIEDSLDEFKVHIESQTLFRQLVKLRERHRIAIRIHNLKSRVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAETVLSMARSLVGSAISKAASAAADETSLLLGVEKDIWYIKDELKTWQAFLRAAELMKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVSSRNTRYSLVKPISSGTEIDMDSYAEDIRNQSARNVDEAELVGFSDSKKR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          348 KPVSISDVAITSTNNHTVAHGEIIDDQSMDADEKKVARKSLTRIRTSVGASEESQLIGRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEISEITHLILNNDSQQVQVISVWGMGGLGKTTLVSGVYQSPRLSDKFVFVTIMRPF
                                              Rice blast fungus; Pyricularia grisea; Magnaporthe grisea;
                Pi-b from rice
                                                                                                                                                                                                                                                                                                                                                                           A blast-resistant gene and related genes, useful grade of high blast resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative 200; Mismatches 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.9%; Score 1204; DB 3; 27.4%; Pred. No. 1.4e-94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---0EFOG---
                                                                                                                                                                                                                                                                       (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
(NORQ ) NORINSUISANSHO NOGYO SEIBUTSU SHIGEN
              blast fungus-resistance protein
                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 26; Page 20-23; 36pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1251 AA;
                                                                 resistance gene
                                                                                                                                 JP2000125885-A.
                                                                                                 Oryza sativa
                                                                                                                                                                                                       29-MAR-1999;
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                                                                                                                                                                     09-MAY-2000
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Matches 353;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----DPSRAGVRGEFKSCRIHDIMRDIAISISREENFILLPEGTDYDVVHGNTRHIAFH 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KDELLKVWAEQIRDLSYDIEDSLDEFKVHIESQTLFRQLVKLRERHRIAIRIHNLKSRVE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVSSRNTRYSLVKPISSGTEIDMDSYAEDIRNQSARNVDEAELVGFSDSKKRLLEMIDTN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANDGPAKVICVVGMGGLGKTALSRKIFESEEDIRKNFPCNAWITVSQSFHRIELLKDMIR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QLLGPSSLDQLLQELQGKVVVQVHHLSEYLIEELKEKRYFVVLDDLW1LHDWNWINEIAF 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PKNNKKGSRIVITTRNVDLABKCATASLVYHLDFLQMNDAITLLLRKTNKNHEDMESNKN 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MQKMVERIVNKCGRLPLAILTIGAVLATKQVSEWEKFYEHLPSELEINPSLEALRRMVTL 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NRSMIQRSRVGIAGKIKTCRIHDIIRDITVSISRQENFVLLPMGDGSDLVQENTRHIAFH 540
                                                                                              Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2 and NBS3, useful for producing plants resistant to Magnaporthe grisea
                                                                                                                                                                                                     The invention comprises the amino acid and coding sequences of nucleotibinding site (NBS) proteins from the Oryza minuta Pi9 locus (bacterial blight and rice blast resistance genes). The DNA sequences may be used markers for resistance to infection with Magnaporthe grisea in plant breeding programs. The present amino acid sequence represents an NBS protein encoded by a gene from the Oryza minuta Pi9 locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAETVLSMARSLVGSAISKAASAAADETSLLLGVEKDIWYIKDELKTMQAFLRAAELMKK
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                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                              98;
                                                                                                                                                                                                                                                                                                                                                         Query Match 26.3%; Score 1384; DB 8; Length 451; Best Local Similarity 51.6%; Pred. No. 5.7e-111; Matches 281; Conservative 73; Mismatches 93; Indels 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English
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                                                                                                                                                                   ID NO 95; 136pp;
                                              2004-121064/12
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                                                                 N-PSDB; ADI57177
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polypeptide and DNA encoding it used to produce plants resistant to 1 blast disease.
                                                                                                                                                                                                              The invention provides a protein which confers resistance to blast disease onto plants. The blast disease-resistance (Pi-b) protein can be expressed by standard recombinant methodology. The novel Pi-b gene is used to produce transgenic plants resistant to the rice blast disease, which will control the disease and increase crop yields. The present sequence represents the rice Pi-b protein. The resistance gene Pi-b is located at the end of the long arm of rice chromosome 2 and displays
                                                                                                                                                                                             Claim 1; Page 8-14; 46pp; English.
                                                          (NORQ ) NAT INST AGROBIOLOGICAL
                                                                                                                   WPI; 2000-064864/06.
N-PSDB; AAZ46679, AAZ46680.
                                                                                                                                                                                                                                                                                                                                 Sequence 1205 AA;
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                                 DLWILHDWNWINEIAFPKNNKKGSRIVITTRNVDLAEKCATAS-LVYHLDFLOMNDAITL 343
                                                LLRKT--NKWHEDMESNKNMQKMVERIVNKCGRLPLAILTIGAVLAT--KQVSEWEKPYE 399
                                                                                                                                              460 VRPKVGMTTKDVGESYFNELINRSMI---QRSRVGIAGK-IKTCRIHDIIRDITVSISRQ 515
                                                                                                                                                                                             ENPVLLPMGDGSDLVQENTRHIA----FHGSMSCKTGL-DWSIIRSLAIFGDRPKSLAHA 570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MLILGALPNLMVLHLYRNAYLGEKLVFK---TG-AFPNLRTLWIYELDQLREIRFEDGSS 902
          ILVELLRSLAEQLHKGSSKKEELLENRVSSKKSLASMEDTELTGQLKRLLEKKSCLIVLD 527
                                                                                                                                                                                                                                                                                                                              631 TLAMPSTYIAALPS---EISKLOCLHTLRCIGOFHYDNFSLAHPMK---CITATICLPKV 684
                                                                                               HLPSELEINPSLEALRRMVTLGYNHLPSHLKPCFLYLSIFPEDFEIKRNRLVGRWIAEGF
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PCRAWVRVWHPFSPRDFVQSLVNQLHATQGVEALLEKEKTEQDLAKKFNGCVNDRKCLIV 228
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                                                                                                                                                                                                                                         DSKKR------LLEMIDTNANDGPAKVICVVGMGG-LGKTALSRKIFESEEDIRKNF
                                                                                                                                                                                                                                                                           DARRAAKQDNQRVDLVQLI--NSEDQDLKVIAVWGTSGDMGQTTIIRMAYEN-PDVQIRF
                                                                                                                                                                                                                                                                                                                                                                                                                                       LNDLSTIEEWDQIKKCFQKCRKGSRIIVSSTQVEVASLCAGQESQASELKQLSADQTLYA
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                                                                               MQAFLRAABLMKKKDELLKVWAEQIRDLSYDIEDSLDBFKVHIESQTLFRQLVKLRERHR
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                                            Gaps
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Query Match

21.1%; Score 1111; UB 34; Local Similarity 26.9%; Pred. No. 1.6e-86;
Matches 334; Conservative 188; Mismatches 351; Indels
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rice, Pi-b gene; blast disease-resistance

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        AIFGDRPKSLAHAVCPDQLRMLRVLDLEDVTFLITQKDFDRIALLCHLKYLSIGYSSSIY 617
                                                                                                                                                                     VGCICATCCLPLL-----CEMYGPLHKALARRDAWTFACCVKPPSIMTGVHEEEG 930
--KQVSEWEKFYEHLPSELEINPSLEALRRMVTLGYNHLPSHLKPCFLYLSIFPEDFEIK 446
                                                            DIIRDITVSISRQENFVLLPMGDGSDLVQENTRHIA----FHGSMSCKTGL-DWSIIRSL 557
                                                                                                                                  RNRLVGRWIAEGFVRPKVGMTTKDVGESYFNELINRSMI---QRSRVGIAGK-IKTCRIH
                                                                          DLMRDIAISKSTEENLVFRVEEGCSAYIHGAIRHLAISSNWKGDKSEFEGIVDLSRIRSL
                                                                                                                                                       --CITNTICLPKVFTPLVSRDDRAKQIAELH--MATKSCWS-------ESIG
                                                                                                                                                                                              AMVPSGIRKLKDLHTLRNINVGR-GNAILRDIGMLTGLHKLGVA--GINKKNGRAFRLAI
                                                                                                                                                                                                                                                                               890 DQLREIRFEDGSSPLLEKIEI-GECRLESGITGIIHLPKLKEIPIRY------GSK
                                                                                                                         SLPRSIGKLOGLOTLNMPSTYIAALPS---EISKLOCLHTLRCIGOFHYDNFSLNHPMK-
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                                                                                                                                                                                                                   EKLSSLQSLHVDAAGISDGGTLECLDSISSPPPLLRTLVLDGILEEMPNWIEQLTHLKKI
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                                                                                                                                     The invention relates to novel broad-spectrum resistance gene Pi2 and the NBS(1-6) genes present in the Pi2 gene cluster region. The rice Pi2-like disease resistance nucleic acid molecules are useful for enhancing disease resistance in plants. The present sequence represents an O. minuta Pi2 gene predicted amino acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --LKEKRYFVVLDDLWILHDWNWINEIAFPKNNKKGSRIVITTRNVDLAEKCATAS-LVY
                                                                                                                                                                                                                                                                                                                                                    MOAFLRAAELMKKKDELLKVWAEQIRDLSYDIEDSLDEFKVHIESQTLFRQLVKLRERHR
                                                                                                                                                                                                                                                                                                                     Gaps
                                that
                                                                                                                                                                                                                                                                                                                   368;
                                nucleic acid molecule that
for creating or enhancing
                                                                                                                                                                                                                                                                                Length 1205;
                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----OELOG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCNAWITVSQSFHRIBLLKDMIRQLLGPSSLDQLL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----SEYLIEE----
                                                                                                                                                                                                                                                                               21.1%; Score 1111; DB 8;
llarity 26.9%; Pred. No. 1.6e-86;
Conservative 188; Mismatches 351;
                               Pi2-like disease resistance resistance in plants, useful
                                                                                                      Disclosure; Fig 5; 120pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----KVVVQVHHL
                                                                   resistance in plants.
WPI; 2004-257576/24
                                                                                                                                                                                                                                                                                             Local Similarity
hes 334; Conserv
                                                                                                                                                                                                                                               Sequence 1205 AA;
                                  rice
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SNLNKLESLSVSSAGMP--GLCGCLDDISSPPENLQSLKTYGSLKTLPEWIKELQHLVKL 1045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is that of the predicted full-length protein encoded by the novel sorghum resistance gene homologue (RGH) S6-1. The invention provides 13 novel maize, sorghum and rice RGH gene femilies (see AAZS8273 e.95) and their protein products (see AAYS842-54). The novel RGH sequences can be used for the production of transgenic plants (and their
                                  673
                                                                                                                        774
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SLFGDWKPFFVYG----KMRFIRVLDFEG-TRGLEYHHLDQIWKLNHLKFLSLRGCYRID
                                               SLPRSIGKLOGLOTLNMPSTYIAALPS---EISKLOCLHTLRCIGOFHYDNFSLNHPMK-
                                                                             --CITNTICLPKVFTPLVSRDDRAKQIAELH--MATKSCWS-------ESIG
                                                                                                 VGCICATCCLPLL------CEMYGPLHKALARRDAWTFACCVKFPSIMTGVHEEEG
                                                                                                                                     EKLSSLQSLHVDAAGISDGGTLECLDSISSPPDLLRTLVLDGILEEMPNWIEQLTHLKKI
                                                                                                                                                                                                               835 YLLRSKLKE-GKTMLILGALPNLMVLHLYRNAYLGEKLVFK---TG-AFPNLRTLWIYEL
                                                                                                                                                                                                                           890 DQLREIRFEDGSSPLLEKIEI-GECRLESGITGIIHLPKLKEIPIRY------GSK
                                                                                                                        VKVPKGIGKLRDLQVLEYVDIRRTSSRAIKELGQLSKLRKLGVTTNGSTKEKCKILYAAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid molecule encoding a resistance gene homolog, useful wcing disease resistant transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          homologue; RGH; transgenic plant; protection.
                                                                                                                                                                                                                                                                                                                     resistance gene homologue 86-1-encoded protein
                                                                                                                                                                                                                                                                                                        ------GQLEGEVN----AHPNRPVL 958
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N-PSDB; AAZS8293, AAZ58294, AAZ58295.
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15-JUL-1999;
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cells, tissues and seeds) having improved resistance to disease. Expression of a novel RGH gene confers disease resistance to a plant by interacting with the complementing phytopathogen avirulence gene product released into the plant by the invading plant pathogen. The methods of the invention find use in controlling plant pests, including fungal pathogens, viruses, nematodes and insects
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231 QK----PDIKKILRHILCQYS----CRECGNNEIWDEQQLINTTRQFLKDKRYFIVIDDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | :: :: | | : | | | : : | | | | | EAIVCASHGAMGSLLWKIGALLSDEYKLLSSVKVDMMFLKAELEVMHAFLKKMSEVEVPD
                                                                                                                                                                                                                                                                                 | | | | :::|:|||||||||: | : | | : | | EQSKCWMKEVRELSYDIEDSIDSFIFSLGCESNSEPRGFKGFVGRCLNLFADAKTRHWIA
                                                                                                                                                                                                                                                                                                                              110 IRIHNLKSRVEEVSSRNTRYSL--VKPISSGTEIDMDSYAEDIRNQSARNVDEAELVGFS
                                                                                                                                                                                                                                                                                                                                                         KKIORLKCHVIEASNRRGRYRVDDAVPRLSRTSID-----PRLPALYTETTRLVGVD
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                                                                                                                                                                                                                                                                 ELLKVWAEQIRDLSYDIEDSLDB--FKVHIESQT------LFRQLVKLRERHRIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    523 MGDGSD--LVQENTRHIA--FHG--SMSCKTGLDWSIIRSLAIFG--DRPKSLAHAVCPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QLRMLRVLDLEDVTFLITQKDFDRIALLCHLKYLSIGYSSSIYSLPRSIGKLQGLQTLNM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AKQIAELHMATKSCWSESIGVKVPKGIGKLRDLQVLEYVDIR-RTSSRAIKELGQLSKLR
                                                                                                                                                                       Gaps
                                                                                                                                                                        167;
                                                                                                                                          DB 3; Length 953;
                                                                                                                                                                       Indels
                                                                                                                                       Query Match 20.2%; Score 1062.5; DB 3; Best Local Similarity 30.0%; Pred. No. 1.8e-82; Matches 320; Conservative 186; Mismatches 393;
                                                                                                           Sequence 953 AA;
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Search completed: February 9, 2005, 08:53:16 Job time : 116.873 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

February 9, 2005, 08:37:57; Search time 28.6479 Seconds (without alignments) 3466.067 Million cell updates/sec Run on:

US-10-656-394A-8 5268 1 MAETVLSMARSLVGSAISKA.....SQVITLITINDSEBIGTAQAG 1032 Title: Perfect Bcore: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
-	961	18.2	926	~	A57072	disease resistance
73	826	15.7	906	~	G96621	probable disease r
e	819	15.5	847	~	T12977	
4	813	15.4		~	T48899	disease resistance
S	803	15.2	_	7	F96573	
9	786	14.9		~	T48898	disease resistance
7	783	14.9		~	F96617	o
ω	116	14.7	831	~	T51185	resistance protein
0	772.5	14.7	835	~	T45590	hypothetical prote
10	768	14.6	820	~	T51186	resistance protein
11	741	14.1	900	N	G96617	probable disease r
12	736.5	14.0	899	~	H96617	probable disease r
13	723.5	13.7	847	~	T12979	hypothetical prote
14	719.5	13.7	839	~	B96538	
15	716.5			~	A86243	
16	969	13.2		~	T08416	w
17	633	•		N	T52429	PRM1 homolog [impo
18	621			~	T52438	
19	612.5			~	T52465	hypothetical prote
20	607.5	11.5		~	T06404	
21	583.5	11.1	1220	N	T06403	resistance complex
22	564		_	N	T07589	disease resistance
23	552	10.5	1255	~	T06267	nematodes resistan
24	549	10.4	-	~	T06269	root-knot nematode
25	538.5	10.2		~	T02213	NBS-LRR type resis
56	477.5	٠.		~	F96637	
27	471	8.9	941	~	B96553	hypothetical prote
28	471	8.9	<del>.</del>	7	T00020	al bli
29	459.5	8.7	483	~	T02226	NBS-LRR type resis

hypothetical prote	PRM1 homolog (impo	resistance to Pseu	hypothetical prote	F7H2.22 protein -	protein T1F9.20 [i	disease resistance	protein F2K11.26 (	protein T3P18.19 [	hypothetical prote	NBS/LRR disease re	hypothetical prote	disease resistance	resistance protein	PRM1 homolog [1mpo	NBS-LRR type resis
T06049	T52440	C86257	G96637	D86293	H96638	T01899	P96659	H96651	E96659	B86257	T05746	A54809	T30558	T52439	T04390
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8.7	9.8	9.6	8.5	8.5	8.4	8.3		8.1	7.9	7.9	7.8	7.7	7.2		6.7

## ALIGNMENTS

335 LOMNDAITLLERKTINKNHEDMESNKAMOKAVERIVNKCGREPLAILTIGAVLATKQV-SE 393

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	DD 64 RNCLEBIKEITYDAEDIIEIFLKGSVNWRSLACFPGGRREIALQITSISKR 115  Qy 119 VEEVSSRNTRYSLVKPĮSSGTEIDMDSYAEDIRNQSARNVDĒAELŲGFSDSKKRĻL 174	DD 116 ISKVIQVMQNLGIKSDIMDGVDSHAQLBRRRELRHFFSSESSENLVGLEKNVEKLV 171  QY 175 -FMIDTNANDGPAKVICVVGMGGLGRTARSKESEBDIRKNFPCNAMITVSQSFHRIE 233	DD 172 ELLYGNDSSHGVSITHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI 290  QY 234 LLKDMIRQLGPSCHQELQGKVVVQVHHLSEYLIEELKEKKYFVVLDDLWILH 290	Db 225KDVWKTILGNLSPKYKDSDLPBDDIQKKLFQLLETKKALIVFDDLWKRE 273  Qy 291 DWNWINBIAFPKNNKKGSRIVITRNVDLAEKCATASLVYHLDFLQMNDAITLLLRKT 348	DD 274 DWYRIAPM-FPE-RKAGWKVLLTSRNDAIHPHCVTFKPELLTHDECWKLLQRIAFSKQKT 331  Qy 349 NKNHEDMESNKNNQKWVERIVNKCGRLPLAILTIGAVLATKQ-VSFWEKFYFHLPSELEI 407	Db 332 ITG?IDKEMVKMAKEMTKHCKLPLAVKLIGGLLDAKHTLRQWKLISHNIV 388  Qy 408NPSLEALRRAWTLGYNHLPSHLKPCFLYLSIFPEPEFIKBNKLVGRWIAEGFV 460	DD 389 GGTSSNENDS-SSVHYLLSLSFEGLPGYLKHCLIYLASYPEDHEIEIERLSYVWAAEGIT 447  Qy 461 RPKVGMTTKDVGESYFNELINRSMIQRSRVGIAGKIKTCRIHDIIRDITVSISRQENF 518	Db 448 YPGNYEGATIRDVADLYIBELVKRNWVISERDALTSRFEKCQLHDLWREICLLKAKENF 507  Qy 519 VLLPMGDGSDLVQENTRHIAFHGSMSCKTGLDWSIIRSLAHFGBRPKSLAHAV 571	Db 508 LQUTDPISSSVHSLASSRSRRLVVYNTSIFSGENDMKNSLRSLLPIPVGYSRFSMGS 567  Qy 572 CPDQLRMLRVLDLEDVTFLITQKDFDRIALLCHLKYLSIGYSSSIYSLFRSIGKLQGLQT 631	DD 568 NFIELPLARVLDLDGARFK-GGKLPSSIGKLIHLKYLSL-YQASVTYLPSSLRNLKSLLY 625  QY 632 LAMPSTYIAALPSEISKLQCLHTLRCIGQFHYDNFSLNHPMKCITNTICLPKVFTPLVSR 691	Qy 692 DDRAKQIAELHMATKSCWSESIGVKVPKGIGKLRDLQVLEYVDIRRTSSRAIKELGQLSK 751	QY 752 LRKLGVTTNGSTKEKCKILYAAIEKLSSLQSLHVDAAGISDGGTLECLDSISSPPPLLRT 811	QY 812 LVLDGILEEMPNWIEQLTHLKKIYLLRSKLKEGKTWLILGALPNLWVLHLYRNAYLGEKL 871 ::	QY 872 VFKTGAFPNLRTLWIYELDQLREIRFEDGSSPLLEKIBIGEC-RLESGITGIHLPKLKE 930   1	Qy 931 IPIRYGSKV 939 :          Db 855 LAIRTNEKV 863	RESULT 3 T12977 hypothetical protein T6H20.240 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
DD 336 LKEDBAWVLFSNKAPPASLEQCRTQNLEPIARKLVERCQGLPLAIASLGSMMSTKKFESE 395  Qy 394 WEKPYEHLPSELEINPSLEALRRWVTLGYNHLPSHLKPCPLYLSIFPEDPEIKRNRLVGR 453	Qy 454 WIAEGFVRPKVGMTTKDVGESYFNELINRSMIQRSRVGIAGKIKTCRIHDIIRDITVSIS 513	Qy 514 RQENFVLLPWGDGSDLVQENTRHIAFHGSMSCKTGLDWSIIRSLAIFGDRPKSL 567 :	Qy 568 AHAVCPDQLRMLRVLDLEDVTFLITQXDFDRIALLCHLKYLSIGYSSSIYSLPRSIGKLQ 627	Qy 628 GLQTLNMPSTYIAALPSEISKLQCLHTLRCIGQFHYDNFSLNHPMKCITNTICLPKV 684	Qy 685 FTPLVSRDDRAKQIAELHWATKSCWSESIGVKVPKGIGKLRDLQVLEYVDIRRTSSRAIK 744	Qy 745 ELGQLSKLRKLGVTTNGSTKEKCKILYAAIEKLSSLQSLHVDAAGISDGGTLECLDSISS 804	Qy 805 PPPLLRTLVLDGILEEMPNWIEQLTHLKKIYLLRSKLKEGKTMLILGALPNLMVLHLYRN 864  1	Qy 865 AYLGEKLVPKTGAPPNLRTLMIYELDQLREIRFEDGSSPLLEKIEIGECRLESGIT 920	Qy 921 GIIHLPKLKEIPIRYGSKVAGLGQLE 946           : ::     ::   bb 872 NLINLQELHLIHVSNQLVERIRGEGSVD 899	RESULT 2 G96621 probable disease resistance protein F23H11.10 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #semience revision 02-Mar-2001	C;Accession: G96621 R;Theologis, A.; Ecker, J.R.; Falm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;	Aduzie, N.T.; hughes, S.; hulzal, D. Nature 408, 816-820, 2000 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,	Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Mu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.	A;Reference number: A86141; MUID:21016719; PMID:11130712 A;Accession: G96621 A;Status: preliminary A;Molecule type: DNA	A;Residues: 1-906 <sto> A;Residues: 1-906 <sto> A;Cross-references: UNIPROT:Q9XIFO; GB:AE005173; NID:g5080812; PIDN:AAD39321.1; GSPDB:GN C;Genetics: A;Gene: F23H11.10 A;Map position: 1</sto></sto>	Query Match 15.7%; Score 826; DB 2; Length 906; Best Local Similarity 27.9%; Pred. No. 8.3e-40; Matches 270; Conservative 182; Mismatches 373; Indels 144; Gaps 34;

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Db 376 EDVKDIVYDADDIIESFLINELRGKEKGIKKQVRTLACFLVDRRKFASDIEGITK 430  Qy 118 RVEEVSERNTRYSLVKPISSGTEIDMDSYAEDIRNOSARNVDEAELVGFSDSKKRL 173	OY 290 HDWININETAFPKNINKGGRIVITTRNVDLAEKCATASLVYHLDFLOMNDAITLLLEKTN 349	Oy 630 QTLNMPSTYIAALPSEISKLQCLHTLRCIGQFHYDNFSLNHPMKCITNTICLPKVFTP 687	T48898 disease resistance protein RPP8 [validated] - Arabidopsis thaliana disease resistance protein RPP8 [validated] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 21-Jul-2000 C;Accession: T48898 and C;Accession: T4898
KDVGESYFNELINRSMIQRSRVGIAGKKTC	Db 615 HLPSTWRILKLLLYILI.  Oy 675 ITNTICLPKVFTPLVSRDDRAKQIAELHWATKSCWSESIGVKVPKGIGKLRDLQVLEYD 734	RESULT 5 FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS FYSETS	Query Match         15.2%;         Score 803;         DB 2;         Length 1584;           Best Local Similarity         27.0%;         Pred. No. 4e-38;         Indels 156;         Gaps 35;           Matches 263;         Conservative 191;         Mismatches 365;         Indels 156;         Gaps 35;           Qy         10 RSLVGSAISKAASAAADETSLLLGVEKDIWYIKDELKTWORFLAAGIMKKKDELKWWA 69;

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33;
A;Accession: T48898
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Nolecule type: DNA
A;Residues: 1-906 <MCD>
A;Cross-references: EMBL:AF089710; NID:g3928861; PIDN:AAC83165.1; PID:g3928862
A;Cross-references: EMBL:AF089710; NID:g3928861; PIDN:AAC83165.1; PID:g3928862
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A;Description: promotes resistance to Peronospora parasitica
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                                                                                                                                                                                       Query Match
14.9%; Score 786; DB 2; Length 906;
Best Local Similarity 25.9%; Pred. No. 1.7e-37;
Matches 257; Conservative 203; Mismatches 347; Indels 1
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probable disease resistance protein F9K23.8 [imported] - Arabidopsis thaliana Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cipate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
CiAccession: F96617
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C., J.; J., Y.; Liu, X.; Liu, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Roomey, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Tile: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: F96617
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                                                                                                                                      GKTWLILGALPNLMVLHLYRNAYLGEKLVPKTGAFPNLRTLWIYELDQLREIRFEDGSSP
                                                                                                                                                                                   783 -DPWPILEKLLHLKSVKLTFKAPAGRRWVCSKGGFTQLCALEISEQSELEBWIVEEGSMP
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61 VVBEIKEIVYDAEDIIETYLLKEKLWKTSGIKMRIRRHACIISDRRRNALDVGGIRTRIS
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14.9%; Score 783; DB 2; Length 907;
Best Local Similarity 26.9%; Pred. No. 2.5e-37;
Matches 256; Conservative 188; Mismatches 391; Indels 116;
                                                                                                                                                                                                                                                                                                           LLEKIEIGEC-RLESGITGIIHLPKLKEIPI
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A;Map position: 1
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Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprotein repeat
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Aate: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 31-Mar-2000
C;Aatesion: T45590
R;Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, submitted to the Protein Sequence Database, December 1999
A;Reference number: Z23008
A;Accession: T45590
A;Status: preliminary
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                                                                                                                                 BSLKR-ALPCNH-EGSRVIITTRIKAVAEGVDGRFYAHKLRFLIFEESWELFEQRAFRNI 343
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KL-LDYBEKNRFIISIFGMGGLGKTALARKLYNS-RDVKERFEYRAWTYVSQEYKTGDIL 233
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                                                       VNVYNDHVAQHSSTTCRREVVHHQVKRYSSEKRKNKRMRSFLNFG-----LDNLVGPDFE
                                                                                                            293 NWINEIAFPKNNKKGSRIVITTRNVDLAEKCATASLVYHLDFLQMNDAITLLLRKTNKNH
                                                                                                                                                                                   EDMESNKNMOKMVERIVNKCGRLPLAILTIGAVLATKOVSEWEKFYEHLPSELEINPSLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRKLGVTTNGSTKEKCKILYAAIEKLSSLOSLHVDAAGISDGGTLECLDSISSPPPLLRT
                                    236 KDMIRQLLGPSS----LDQLLQELQGKVVVQVHHLSEYLIEELKEKRYFVVLDDLWILHDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                575 QLRMLRVLDLEDVTF-LITQXDFDRIALLCHLKYLSI-GYSSSIYSLPRSIGKLQGLQTL
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A;Residues: 1-835 <CHO>
A;Cross-references: EMBL:AL133314
A;Experimental source: cultivar Columbia; BAC clone F12A12
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A, Note: F12A12.5C
C, Superfamily: di
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Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprotein repead
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resistance protein RPP13 [imported] - Arabidopsis thaliana
c;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 02-Sep-2000
C;Accession: TSI185
R;Pittner-Eddy, P.D; Crute, I.R.; Holub, E.B.; Beynon, J.L.
Plant J. 21, 177-188, 2000
A;Pittle: RPP13 is a simple locus in Arabidopsis thaliana for alleles that specify chitle: RPP13 is a simple locus in Arabidopsis chaliana for alleles that specify chitle: TSI185
A;Accession: TSI185
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-831 <BIT>
A;Residues: 1-831 <BIT>
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                                                                                                                  FLITQKDFDRIALLCHLKYLSIGYSSSIYSLPRSIGKLQGLQTLNMPSTYIAALPSEISK 648
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                                                                                                                                                                                                                                                                                                                                                    669 KKTRLS------LRNLVKLETLVYFSTWHSSSKDLCGMTRLMTLAIRLTRVT- 714
                                                                                                                                                                                                                                                                                                                                                                                         765 EKCKILYAAIEKLSSLQSLHV---DAAGISDGGTLECLDSISSPPPLLRTLVLDGILEEM 821
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                                         RTLWIYELDQLREIRFEDGSSPLLEKIEIGECRLESGITGIIHLPKLKEIP 932
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A,Experimental source: cultivar Rld
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C,Superfamily: d
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A;Gene: RPP13
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                                                                                      EVSSRNTRY---SLVKPISSGTEIDMDSYAEDIRN-QSARNVDEAE-LVGFSDSKKRLLE 175
                                                                                                                                          MIDTNANDGPAKVICVVGMGGLGKTALSRKIFESEBDIRKNFPCNAMITVSQSFHRIBLL 235
                                                                                                                                                                                                                                          289 KR-ALPCNH-EGSRVIITTRIKAVAEGVDGRFYAHKLRFLTFEESWELFEQRAFRNIQ-- 344
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                                                                                                                                                                                                                                                                                                                                             104 IVPDLSFKELRHESKLCPLYLSIFPEDYEIDLEKLIHLLVAEGFIQGDEEMMEDVARXY 463
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                                                                                                                                                                                                                             KDMIRQLLGPSSLDQLLQELQGKVVVQVHHLSEYLIBELKEKRYFVVLDDLWILHDWNWI 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YNDHVAQHSSTTCRREVVHHQPKRYSSEKRKNKRMRSFLYFGE----FDHLVGLDFETLK 564
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                      MARSLVGSAISKAASAADETSLLLGVEKDIWYIKDELKTMQAFLRAABLMKKKDELLKV
                                      165;
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354; Indels
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266; Conservative
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RESULT 10
T51186
C:species: Arabidopsis thaliana (mouse-ear cress)
C;Species: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 09-Jul-2004
C;Accession: T51186
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A,Map position: 3
C,Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprotein repeat
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Ribittner-Eddy, P.D.; Crute, I.R.; Holub, B.B.; Beynon, J.L.
Plant J. 21, 177-188, 2000
A;Fittle: RPP13 is a simple locus in Arabidopsis thaliana for alleles that specify A;Reference number: 225333
A;Reference number: 225333
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llarity 27.6%; Pred. No. 1.6e-36;
Conservative 170; Mismatches 346; Indels 162;
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nes 259; Conserv
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PB 774 SEGGHGRIRGLKIF-INRIDDIGIEERAWPHILINV 809  PRESULT 11  G96617  TO SEGGRIRGLKIF-INRIDDIGIEERAWPHILINV 809  G96617  C1020e18 Arabidopsis thaliama (mouse-car cress)  C1020e18 Arabidopsis (mouse-car cress)  C1020e18 Arabidopsis (mo	455 IRDUGESYLEELANERNOVILAREACHLHOWRENCLIKAKEBRENGLAGIPE 514  OY 524 GDOEDLYORDRIPHIA——
TUANDGPAKVICVGMGGLGKTALSRKIFESEEDIRKNFPCNAWITVSQSFHRIELLKDM 238  : :::	A,Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  A,Fdcession: H96617 A,Status: preliminary A,Molecule Vype: DNA A,Rolecule Vype: DNA A,Gone: F9K23.6 A,Gone: F9K23.6 A,Gone: F9K23.6 A,Gone: F9K23.6 A,Map position: 1  Query Match Best Local Similarity 25.2%; Pred. No. 1.2e-34; Best Local Similarity 25.2%; Pred. No. 1.2e-34; Matches 241; Conservative 200; Mismatches 391; Indels 123; Gaps 28; Matches 241; Conservative 200; Mismatches 391; Indels 123; Gaps 28; Matches 241; Conservative 200; Mismatches 391; Indels 123; Gaps 28; Matches 241; Conservative 200; Mismatches 391; Indels 123; Gaps 28; Matches 241; Conservative 200; Mismatches 391; Indels 123; Gaps 28; Matches 241; Conservative 200; Mismatches 391; Indels 123; Gaps 28; Matches 241; Conservative 200; Mismatches 391; Indels 123; Gaps 28; Matches 241; Conservative 200; Mismatches 391; Indels 123; Gaps 28; Matches 241; Conservative 200; Mismatches 391; Indels 123; Gaps 28; Matches 241; Conservative 200; Mismatches 391; Indels 123; Gaps 28; Matches 241; Conservative 200; Mismatches 391; Indels 123; Gaps 28; Matches 241; Conservative 200; Mismatches 241; Indels 200; Mismatches 241; Indels 200; Mismatches 241; Indels 200; Mismatches 241; Indels 200; Mismatches 241; Indels 200; Mismatches 241; Indels 200; Mismatches 241; Indels 200; Mismatches 241; Indels 200; Mismatches 241; Indels 200; Mismatches 241; Indels 200; Mismatches 241; Indels 200; Mismatches 241; Indels 200; Mismatches 241; Indels 200; Mismatches 241; Indels 200; Mismatches 241; Indels 200; Mismatches 241; Indels 200; Mismatches 241; Indels 200; Mismatches 241; Indels 200; Mismatches 241; Indels 200; Mismatches 241; Indels 200; Mismatches 241; Indels 200; Mismatches 241; Indels 200; Mismatches 241; Indels 200; Mismatches 241; Indels 200; Mismatches 241;

DB 2; Length 847; IndelB 9

239

299 287 479

652

514

712

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A;Gene: ATSP:T6H20.260
A;Map position: 3
C;Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprotein repeat
                                                                                                                                                                                                                                                                             WAEQIRDLSYDIEDSLDEFKVHIESQTLFRQLVKL-----RERHRIAIRIHNLKSRVE 120
                                                                                                                                                                                                                                                            EVSSRNTRYSLVKPISSGTEIDMDSYAEDIRNQSARNVDEAE-LVGFSDSKKRLLEMIDT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                            ELOKIGKEMVOKCGGLPRITVVLAGLMSRKKPNEWNDVW----SSLRVKDDNIHVSSLFD 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       480 INRSMIQ----RSRVGIAGKIKTCRIHDIIRDITVSISRQENFVLLPMGDGSDLVQENTRH 536
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                                                                                                                                                                                                                    DGGDNKIYMISIFGMEGLGKTSLARKLFNS-SDVKESFEYRVWTNVSGECNTRDILMRII
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A;Experimental source: cultivar Columbia; BAC clone T6H20
C;Genetics:
                                                                                           Query Match 13.7%; Score 723.5; DB 2; Best Local Similarity 27.0%; Pred. No. 6.3e-34; Matches 249; Conservative 178; Mismatches 382;
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Dispectical protein T6H20.260 - Arabidopais thaliana

CiSpecies: Arabidopais thaliana (mouse-ear cress)

CiSpecies: Arabidopais thaliana (mouse-ear cress)

CiSpecies: 13-Aug-1999 #text_change 09-Jul-2004

CiAccession: T12979

Richoisen, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, submitted to the Protein Sequence Database, July 1999

A;Reference number: 217586

A;Accession: T12979

A;Residues: 1-847 cCHO>
       238 TSKERKD----EIQNMKEADLH---DDLFRLLESSKTLIVLDDIWKEEDWDLIKPI-FPP 289
                                                                                                                                                                                                                 NNKKGSRIVITTRNVDLAEKCATASLVYHLDFLQMNDAITLL--LRKTNKNHEDMESNKN 360
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                                                   RNTRYSLVKPISSGTEID--MDSYAEDIRNQSARNVDEAELVGFSDSKKRLLEMIDTNAN 182
                                                                                                                      XDDYQIVSLTGMGGLGKTTLARQVF-NHDVVKDRFDGFAWVSVSQEFTRISVWQTILQNL 237
                                                                                                                                                           LGPSSLDQLLQELQGKVVVQVHHLSEYLIEELKEKRYFVVLDDLWILHDWNWINEIAFPK 302
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                                                                   DMQSFGVQQIITDGSRSSHPLQERQREMRHTFSRD-SENDFVGMEANVKKLVGYL---VE
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RESULT 14 B96538 hypothetical protein F1413.19 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 C;Accession: B96538 C;Date: OL, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L. A;Authors: Huuther, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Accession: B96538 A;Accession: B96538 A;Accession: B96538 A;Accession: B96538 A;Acsidues: 1-839 - <sto- -<sto-="" 1<="" a;accession:="" a;gene:="" a;map="" b39="" f1413.19="" position:="" td=""><td>Query Match Beet Local Similarity 25.64; Pred. No. 1.18-33; Beet Local Similarity 25.64; Pred. No. 1.18-33; Beet Local Similarity 25.64; Pred. No. 1.18-33; Beet Local Similarity 25.64; Pred. No. 1.18-33;  MARSINGSAISKAASAADETSILLGYRDIWIIKDELKTHORILARAHELMKKKDELLKV 67                                       </td></sto->	Query Match Beet Local Similarity 25.64; Pred. No. 1.18-33; Beet Local Similarity 25.64; Pred. No. 1.18-33; Beet Local Similarity 25.64; Pred. No. 1.18-33; Beet Local Similarity 25.64; Pred. No. 1.18-33;  MARSINGSAISKAASAADETSILLGYRDIWIIKDELKTHORILARAHELMKKKDELLKV 67

Oy       246         Oy       301         Oy       301         Oy       361         Oy       416         Oy       475         Oy       502         Oy       561         Oy       561         Oy       561         Oy       644         Oy       644         Oy       644         Oy       628         Oy       638         Oy       663         Oy       683         Oy       762         Oy       762         Oy       730         Oy       787	SSLDQLLQELQGKVVVQVHILSEXLIEBLKEKRYFVVLDDLWILHDWNWINEIAF 300 :	PKNNKKGSRIVITTRNVDLAEKCATASLVYHLDFLQMNDAITLLLRKTNKNHEDMESNKN 360  :  :  ::: :   : :::  PRKRGWKWLLTSRNEGVGIHADPKSFGFKTRILTPRESWKLCEKIVFHRRDETGTLSD 321	MQKMVERIVNKCGRLPLAILTIGAVLATKQ-VSEWEKFYEHLPSELEINPSLEALR 415  :	RMVTLGYNHLPSHLKPCFLYLSIFPEDFEIKRNRLVGRWIABGFVRPK-VGWTTKDVGES 474  :::    :	YFNELINRSMIQRSRVGIAGKIKTCRIHDIIRDITVSISRQENFV-LLPMGDGSDLVQ 531    -  -  -  -  -  -  -  -  -  -  -  -  -	ENTRHIAFHGSMSCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLD 583	LEDVTPLITQKDFDRIALLCHLKYLSIGYSSSIYSLPRSIGKLQGLQTLNMPSTYIAALP 643	SEISKLOCLHTLRCIGOFHYDNFSLNHPMKCITNTICLPKVFTPLVSRDDRAKQI-AELH 702 	MATKSCWSESIGVKVPKGIGKLRDLQVLEYVDIRRTSSRAIKELGQLSKLRKLGV-TTNG 761 	STKEKCKILYAAIBKUSSLQSLHVDAAGISDGGTLECLDSISSPPPLLRTLVVD 815 	GILEEMPNWIEQLTHLKKIYLLRSKLKEGKTWLILGALPNLMVLHLYRNAYLGEKLV 872 	FKTGAFPNLRTIMIYELDQLREIRFEDG 900            :     :
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
NBS-LRR disease resistance protein homologue.
Name=rga S-9202;
Hordeum vulgare (Barley).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
NCBI_TaxID=4513;
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MEDLINE=25600677; PubMed=12715163;

MEDLINE=25600677; PubMed=12715163;

A Krussell L., Jensen J., Waterman E.H., Jahoor A., Pryor A.J.,

Langridge P., Schulze-Lefert P., Stougaard J.;

Tamarley disease resistence gene analogs of the NBS-LRR class:

I dentification and mapping.";

Mol. Genet. Genomics 269:150-161(2003).

R Mol. Genet. Genomics 269:150-161(2003).

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R Mol. Genet. Genomics 269:150-161(2003).

R GO; GO:0005524; F:ATP binding! IEA.

GO; GO:0005915; P:apoptosis; IEA.

GO; GO:00042829; P:adefense response to pathogen; IEA.

InterPro; IPR000767; Disease_resist.

InterPro; IPR00912; Naha_NRC.

InterPro; IPR00913; NB-ARC.

InterPro; IPR00914; NB-ARC; 1.

R PRINTS; PR0034; DISEBASESIST.

R PRINTS; PR0034; DISEBASESIST.
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Q6zd15
Q6zb314
Q9zsb2
Q9zsb2
Q6x4c9
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Q7xyb9
Q84zm1
Q81jz8
Q6zd74
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06X4U3
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(c) 1993 - 2005 Compugen Ltd.
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2: uniprot_trembl:*
                                                                          protein search, using
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seq length: 200000000
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                                                                                                                                                                                                                                                                             KDELLKVWAEQIRDLSYDIEDSLDEFKVHIESQTJFRQLVKLRERHRIAIRIHNLKSRVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SQLIGHES ----LKRFEGK-PIRAHDLGTHLRDGLKELRYFVVFDDLWNTDHWEWIREFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESIGVKVPKGIGKLRDLQVLEYVDIRRTSSRAIKELGQLSKLRKLGVTTNGSTKEKCKIL
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                                                                                                                                                                  Length 1007;
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                     IEA
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48.2%; Score 2539; DB 2;
Best Local Similarity 53.6%; Pred. No. 3.5e-127;
Matches 548; Conservative 152; Mismatches 291;
                   to pathogen;
GO; GO:0006915; P:apoptosis; IEA.
GO; GO:0042829; P:defense reaponse t
InterPro; IPR000767; Disease_resist.
InterPro; IPR002182; NB-ARC.
                                                                              PFam, PF00931, NB-ARC, 1.
PRINTS, PR00364, DISEASERSIST.
SEQUENCE 1007 AA, 114793 MW;
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                                                                                                           CRNORYSNYFDNEDSCERWFNIVCMPLVLAS--EPDQRASFFAELPMACSTGFGFPKSYG
  QLLGPSSLDQLLQELQGKVVVQVHHLSEYLIEELKEKRYFVVLDDLW1LHDWNW1NE1AF
                        PKNNKKGSRIVITTRNVDLAEKCATASLVYHLDFLQMNDAITLLLRKTNKNHEDMESNKN
                                                                                                                                                                      MOKMVERIVNKCGRLPLAILTIGAVLATKQVSEWEKFYEHLPSELEINPSLEALRRMVTL
                                                                                                                                                                                              NRSMIQRSRVGIAGKIKTCRIHDIIRDITVSISRQENFVLLIPMGDGSDLVQE-NTRHIAF
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01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Similar to gene for Pib.
Oryza sativa (japonica cultivar-group).
Briaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Bhrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Sasaki T., Matsumoto T., Yamamoto K.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP001068 BAA90798.1; -.
Gramene, OBLWW7; -.
GO; GO:0005524; F:ATP binding; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               465 IRRGPLVRRWIAEGFVNQRHGLSMEEVAESYFDEFVARSIVQPVKIDWSGKVRTCRVHDM
                                                           IRDITVSISRQENFVLLPMGDGSDLV-QENTRHIAFHGSMSC--KTGLDWSIIRSLAIFG
                                                                                                                                                            562 DRPKSLAHAVCP---DQLRMLRVLDLEDVTFLITQKDFDRIALLCHLKYLSIGYSSSIYS
                                                                                                                                                                                                                                                            LPRSIGKLOGLOTLNMPSTYIAALPSEISKLOCL-HTLRCIGOFHYDNFSLNHPMKCITN
                                                                                                                                                                                                                                                                                                                                                                                                              684 T------GSVKCFRPDSGLEMTAGVVKNMMALQSLAHIVVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NLMVLHLYRNAYLGEKLVFKTGAFPNLRTLWIYELDQLREIRFEDGSSPLLEKIEIGECR
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Espermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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llarity 32.5%; Pred. No. 2.1e-57;
Conservative 189; Mismatches 356; Indels 144;
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Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005828; BAD46435.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequenc
25-OCT-2004 (TrEMBLrel. 28, Last annotat
Similar to NBS-LRR type resistance gene.
Name=P0702F05.14;
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Matches 331;
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                                                                                NAHPNRPVLLMYSDRRYHDLGAEAEGSSIEVQTADPVPDAEGSVTVAVEATDPLPEQEGE 1009
SELRGIRFEKDALPHMERMEIECCQLRSGIVGIKHLEQLNEISL--GCDVAGLDLLEQEV 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KDELLKVWAEQIRDLSYDIEDSLDEFKVHIESQT----LFRQ----LVKLRERHRIAIRIH 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NLKSRVEEVSSRNTRYSLVKPISSGTEIDMDSYAEDIRNQSARNVD------EAELV 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271 IEELKEKRYFVVLDDLWILHDWNWINEIAFPKNNKKGSRIVITTRNVDLAEKCATA--SL 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VYHLDFLQMNDAITL-LLRKTNKNHEDMESNKNMQKMVERIVNKCGRLPLAILTIGAVLA 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         445 IKRNRLVGRWIAEGFVRPKVGMTTKDVGESYFNELINRSMIQRSRVGIAGKIKTČRIHDI 504
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                                                                                                                  952 KAHPKTPALRLLQDRSKIDLGLPV-----VLTKD-----EGS-NVEERAKESVHDDAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza Bativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartodeae, Oryzeae, Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.6%; Score 1294.5; DB 2; Length 953; larity 33.3%; Pred. No. 1.1e-60; Conservative 207; Mismatches 342; Indels 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sasaki T., Matsumoto T., Yamamoto K.; "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, clone:P0702F05.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005828; BAD46438.1; -. SEQUENCE 953 AA; 108557 MM; DAFD5081E707261C CRC64;
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Last annotation update)
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25-OCT-2004 (TrEMBLrel. 28, Last sequenc
25-OCT-2004 (TrEMBLrel. 28, Last annotat
Similar to NBS-LRR type resistance gene.
Name=P0702F0S.17;
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Best Local Similarity
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               HILDEKEHSLSLDNLAFVESPPLFITKFSLAGELERLPPWIPSLRNVSRFALRRTEL-HA
                                                                                                                                                                                                                                                                                                                                                                                                      LERLILSFLREPKYGISGLENLPKIKEIEF-FGDIILSVVTKVASC-----VKAHPNHP
        AELVGFSDSKKRLLEMIDTNANDGPAKVICVVGMGGLGKTALSRKIFESEEDIRKNFPCN
                                                                      QVHHLSEYLIBELKEKRYFVVLDDLWILHDWNWINEIAFPKNNKKGSRIVITTRNVDLAE
                                                                                                     KCAT--ASLVYHLDFLOMNDAITLLLRKTNKNHEDMESNKNMQKMVERIVNKCGRLPLAI
                                                                                                               LTIGAVLATK---QVSEWEKFYEHLPSELEINPSLEALRRMVTLGYNHLPSHLKPCFLYL
                                                                                                                                                                   SIFPEDFEIKRNRLVGRWIAEGFVRPKVGMTTKDVGESYFNELINRSMIQRSRVGIAGKI
                                                                                                                                                                                                   KTCRIHDIIRDITVSISRQENFVLLPMGDGSDLV-QENTRHIAFHGS--MSCKTGLDWSI
                                                                                                                                                                                                                                  IRSLAIFGDRPKSLAHAVCP---DQLRMLRVLDLEDVTFLITQKDFDRIALLC---HLKY
                                                                                                                                                                                                                                                                 LSIGYSSSIYSLPRSIGKLQGLQTLNMPSTYIAALPSEISKLQCLHTLRCIGQFHYDNFS
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                                       AWITVSQSFHRIELLKDMIRQLLGPSSLDQLLQE-----
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                                                                             01-MAR.2003 (TrEMBLrel. 23, Created)
01-MAR.2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative disease resistance protein RPH8A.
Name=0J1634 B10.108;
Oryza sativa (japonica cultivar-group).
Bukaryota, Viridaplantes, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                PRT; 1494
                                                PRELIMINARY;
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**Q8H5A7** 

RESULT 5

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 KDELLKVWARQIRDLSYDIEDSLDEFKVHIESQT-----LFRQ----LVKLRERHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IAIRIHNLKSRVEEVSSRNTRYSLVKPISSGTEIDMDSYAEDIRNQSARNVD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----FHEYDRAYEI-----KPLTDCESRDLFFKRIFGSSICPEHLEDISAKILGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 23.3%; Score 1225.5; DB 2; Length 1494; Best Local Similarity 32.4%; Pred. No. 9.8e-57; Matches 332; Conservative 188; Mismatches 361; Indels 145;
                     BAC
                                                                                                                                                                                                                                                                                                                                                                                                        168313 MW; 15BB15F247C3446B CRC64;
                                                               Submitted (JŪL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003840; BAC15497.1; -.
Sasaki T., Matsumoto T., Yamamoto K.; "Oryza sativa nipponbare(GA3) genomic DNA, chromosome
                                                                                                                                                                      pathogen; IEA
                                                                                                       Gramene; Q8H5A7; -
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005915; P:apoptcosis; IEA.
GO; GO:0042829; P:defense response to l
InterPro; IPR000767; Disease_resist.
InterPro; IPR001611; IER.
InterPro; IPR001621; NB-ARC.
                                                                                                                                                                                                                                                   InterPro; IPR002885; PPR.
InterPro; IPR008940; Prenyl_trans.
                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00364; DISEASERSIST.
TIGREAMB; TIGR00756; PPR; 4.
                                                                                                                                                                                                                                                                                               Pfam; PF00560; LRR 1; 3.
Pfam; PF00931; NB-ĀRC; 1.
Pfam; PF01535; PPR; 4.
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119 RAKVEDVSQRNMRYHGVSAAAPQSSSVTAAELLQSTAAIDDIDEARRAAKQOEKVDLVKL   178   179   171   170   174   174   175   176   176   176   177   176   177   177   177   177   177   177   177   177   177   177   177   177   177   177   177   178   178   178   178   178   179   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170	267GEYLIEBLKBKRYEVVLDDLMILHDMNNINBIAFPKNNKKGSRIVITTRND 318 530 STWGSEBLIDCKACDLTCKKYLIVLDDLSTTTEMDSIIR-NLFINN-NGSRILLTTRFKL 531 JACHCSKZARAL-VYHLDFLQMNDATTLLRKTNKNHEDMSSNKRMQRAVERIVKKCGRLPL 531 JACKCATASL-VYHLDFLQMNDATTLLRKTNKNHEDMSSNKRMQRAVERIVKKCGRLPL 54 JACKTACATASL-VYHLDFLQMNDATTLLRKTNKNHEDMSSNKRMQRAVERIVKKCGRLPL 55 WAALVGGPLSARPRNIEGETDODALBLPTTKTRMGDSSELKPDLKEEAAXIIKKCCRLPL 56 WAALVGGPLSARPRNIEGETDODALBLPTTKTRMGDSSELKPDLKREAAXIIKKCCRLPL 57 WAILTGAVLATKQVSBWEKEYBHLPSELEBINPSLEALRRWYLCGYHLPGSCFLY 56 TATTGAVLATKQVSBWEKEYBHLPSELEBINPSLEALRRWYLCGYHLFGSCFLY 57 WAILTGAVLATKQVSBWEKEYBHLPSELEBINPSLEALRRWYLCGYHLFGSCFLY 56 TATTGAVLATKQVSBWEKEYBHLPSELEBINPSLEALRRWYLCGYHLFGSCFLY 57 WSITRSLINDITVSISRQENPYLLDMGDSDLVQBNTRHIAFHGSWSCKTGLD 55 WSITRSLINDITVSISRQENPYLLDDBLTGSRSWRCHBQNSCKTGLD 55 WSITRSLINDITVSISRQENPYLLDDBLTGSRSWRCHBQNSCKTGLD 56 TGPCQYYNLWHEIIISKSEBEHVLYVLDDBLTGSRSWRCHBQNSCKTGD 57 WSITRSLINDITVSISRQENPYLLDDBLTGSRSWRCHBQNSCKTG
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711 BSI---GVKVPKGIGKLRDLQVLEYVDIRRTSSRAIKELGQLSKLRKLGVTTNGSTKEKC 767
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VRQFKANSREGTGKTPQGTPSGVSVLNEMEAQDYNLLHDFTGYVTNKKYLVVLNGLSTIE 298
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                                                                                                                       EWDWIKTYLPNNHNGSRVLVCTQQAEVASCCTCTDDKYKVSEIQHEGSFSKPLYVFYKEV 358
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                                                                          MB------
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                                                                                                                                                                                                                                                                       ----AKVICVVGMGGLGKTALSRKIFESEE
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                                                                                                                                                                                                                   359 VSQPVNSDSTKMKSETRSSMEGASTTSDSKTVPSDGVIQEDGPKDLPESSLPPHLNRDSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58
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RAKVEDVSQRNMRYHGVSAAAPQSSSVTAAELLQSTAAIDDIDEARRAAKQQEKVDĽVKL
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                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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resistance
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STRAIN=Tohoku IL-9; TISSUE=Green leaf;
STRAIN=21882385; PubMed=11725950; DOI=10.1023/A:1012457113700;
MEDLINES=21882385; PubMed=11725950; DOI=10.1023/A:1012457113700;
WADA Z.X., Yamanouchi U., Katayose Y., Sasaki T., Yano M.;
"Expression of the Pib rice-blast-resistance gene family is upregulated by environmental conditions favouring infection and by chemical signals that trigger secondary plant defences.";
Plant Mol. Biol. 47:653-661(2001).
EMBL; AB013451; BAA93618.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              389;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.0%; Score 1209.5; DB 2; Length ilarity 27.4%; Pred. No. 5.3e-56; Conservative 197; Mismatches 347; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F45F3EBCF9F0251A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Tohoku IL-9; TISSUE-Green leaf;
MEDLINE=99348180; PubMed=10417726;
Wang Z., Yano M., Yamanouchi U., Iwamoto M., Monna L.,
Katayose Y., Sasaki T.;
The Pib gene for rice blast resistance belongs to the
binding and leucine-rich repeat class of plant disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pathogen; IEA.
                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                    PRT; 1226 AA
                                                      1199 YDQTYTEFKEQLQKQLDMNKNKPNL 1223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gramene; Q9MBF2; -. GO; GO: 0005524; F: ATP binding; IEA. GO; GO: 0006515; P: apoptosis; IEA. GO; GO: 00048829; P: defense response to InterPro; IPR000767; Disease_resist. InterPro; IPR001611; IRR.
                                  ------QLEGEVNAHPNRPVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KSRVEEVSSRNTRY------
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SEQUENCE 1226 AA; 138086 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002182; NB-ARC.
                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00560; LRR 1; 3.
Pfam; PF00931; NB-ARC; 1
                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genes.";
Plant J. 19:55-64(1999)
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                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (Rice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 352; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                    PibH8 protein.
Name=PibH8;
                                                                                                                                                                                                                                                 01-OCT-2000
01-OCT-2000
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COMBR2

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LGALPNLMVLHLYRNAYLGEKLVFKTGAFPNLRTLWIYBLDQLRBIRFEDGSSPLLEKIE 909
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                                                                                                                                                                                                                                                                                                                                    731 EYVDIRRISSRAIKELGQLSKLRKLGVTTNGSTKEKCKILYAAIEKLSSLQSLHVDAAGI 790
       MVLQIILSKSIEENQLFIIKKHCNEVPQSKIRHLVVSRWKRRDERLENINFSYVRSLTVF 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 KD-ELLKVWARQIRDLSYDIEDSLDEFKVHIESQTLFRQLVKLRERHRIAIRIHNLKSRV 119
                                                                           -SPQNLRYLETLDIQDTKVTQLPDGIAKLEKLRYL----LAGVNFSKE-----L
                                                                                                                                                                                                                                        LPKVFTPLVSRDDR-AKQIAELHMATKSCWS-----BSIGVKVPKGIGKLRDLQVL
                                                     GDRPKSLAHAVCPDQLRMLRVLDLEDVTFLITQKDFDRIALLCHLKYLSIGYSSSIYSLP
                                                                                                                                                                                                                                                                     SDGGTLECL-DSISSPPPLLRTLVLDGILEEMPNWIEQLTHLKKIYLLRSKLKEGKTMLI
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gene Lr10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poalea; Poaceae; Pooldeae;
Triticeae; Triticum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=14645721; DOI=10.1073/pnas.2435133100; PubMed=14645721; DOI=10.1073/pnas.2435133100; PubMed=14645721; DOI=10.1073/pnas.2435133100; PubMed=14645721; DOI=10.1073/pnas.243513100; Parallilet C., Travella S., Stein N., Albar L., Nublat A., Kell from the hexaploid wheat (Triticum aestivum L.) genome."; Proc. Natl. Acad. Sci. U.S.A. 100:15253-15258(2003).

BENBL; AZ720159; AAQ01786.1; -
GO; GO:0005524; PATP binding; IEA.
GO; GO:0005524; PatP binding; IEA.
GO; GO:0005815; P:apoptosis; IEA.
GO; GO:0005829; P:defense response to pathogen; IEA.
InterPro; IPR001611; IRR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1169 AA; 131589 MW; A64B186A3664C6CA CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Triticum aestivum (Wheat).
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Pfam; PF00931; NB-ĀRC; 2
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       208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVGPSDSKKRLLEMIDTNANDGPA-----KVICVVGMGGLGKTALSRKIFESEEDIRKN 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         271 YLREKRYVIIVDDLHSREEWEHIWPV-LHVDGGKGSRVVVTTRREDVARHCAGLVREGHG 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 KASVEELNORFLRYRIVVEHPRASRGGASDDQQQLHDHDGQYYSAELAFQ-----ESD 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                328 LVYHLDFLOMNDAITLLLRKTNKNHEDMESNKNMQKMVERIVNKCGRLPLAILTIGAVLA 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HVYELRPLGREESKOLFCQKVYKSTEY1-LEKEMEDLAGPILKRCRGLPLAISTIGGLLA 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KRNRLVGRWIAEGFVRPKVGMTTKDVGESYFNELINRSMIQ--RSRVGIAGKIKTCRIHD 503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPCNAWITVSQSFHRIELLKDMIRQLLGPSSLDQLLQELQGKVVV----QVHHLSEYLIE
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                                                                                                                                                                                     Oryza sativa (japonica cultivar-group).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Match 22.9%; Score 1209; DB 2; Length 963; Local Similarity 33.0%; Pred. No. 4.1e-56; les 335; Conservative 209; Mismatches 348; Indels 124;
                                                                                                                                                                                                                                                                                                                                                                                  BAC
                                                                                                                                                                                                                                                                                                                                              SERGIT T. MATERIANCE T., KATAYOSE Y.;
"OTYZA GATIVA NIDRONDATE (GA3) genomic DNA, chromosome 9, BAC Clone:OSJNBb0034B12.";
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005735; BAJ3830.1;
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0006915; P:Apoptosis; IEA.
GO; GO:000415; P:Apoptosis; IEA.
InterPro; IPR000767; Disease_resist.
InterPro; IPR00161; LRN.
InterPro; IPR00161; LRN.
InterPro; IPR00161; LRN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       963 AA; 109012 MW; 5E808C349CBFA3C6 CRC64;
                                                                                         Last sequence update)
Last annotation update)
                          963 AA
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                                                                        Created)
                          PRT;
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                                                                   25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                       Putative registance protein.
Name=OSJNBb0034B12.23;
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Pfam; PF00931; NB-ARC; 1
                          PRELIMINARY:
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DVSQRNVRYHLIKGSAKAT-----INSTEQSSVIATAIFGIDDARRAAKQDNQRV 170
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                                                                                                                                                                                                                                                                                                                                     Oryza sativa (Rice).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Tohoku IL-9; TISSUE-Green leaf;
MEDLINE=99348180; PubMed=10417726;
MEDLINE=99348180; Yubmed=10417726;
Mang Z., Yano M., Yamanouchi U., Iwamoto M., Monna L., Hayasaka H. Katayose Y., Sasaki T.;
"The Pib gene for rice blast resistance belongs to the nucleotide binding and leucine-rich repeat class of plant disease resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nakamura S., Motomura T.,
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SEQUENCE 1251 AA; 141638 MW; 011F56630118AB98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pathogen; IEA
                                                                                                                                                                                                                                                                        Last annotation update)
                                                                                                                                                                                                                            Created)
Last sequence update)
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1138 RAGTELEREARLKEQFRTQLARNPKKPILKM 1168
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                                                                                                                                                                               1251
                     ------QLEGEVNAHPNRPVLLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gramene; Q9ZNV6; --
GO; GO:0005524; F:APP binding; IEA.
GO; GO:0005915; P:apoptosis; IEA.
GO; GO:0042829; P:defense response to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000767; Disease_resist.
InterPro; IPR001611; LRR.
InterPro; IPR002182; NB-ARC.
                                                                                                                                                                                                                                               Last
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STRAIN=BL-1; TISSUE=Green leaves;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jwa N., Tsunoda Y., Akiyama K.,
Kodama O., Kawasaki S.;
Submitted (APR-1999) to the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB013449; BAA76282.2;
EMBL; AB011448; BAA76281.2;
EMBL; AB026839; BAA85975.1;
Gramene; QSSXV0;
                                                                                                                                                                                                  Q9ZNV6; Q9SSY0;
01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                   Name=PIB; Synonyms=Pi-b;
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Pfam; PF00931; NB-ARC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genes.";
Plant J. 19:55-64(1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4530;
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Matches 353; C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    520 TRVEDIGKHCSKKRKNIYKLQGLELNDAHDLFIQKVFDKTMDLDEQYPELVEQTNMILKK 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CKGLPLAIVTIGGFLANOPKTALEWKKLNEHISAAELQMNPELEAIITVLNKSYDGLPYH 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         767 CKILY-AAIEKLSSLQSLHVDAAGISDGGTLECLDSISSPPPLLRTLVLDGILEEMPNWI 825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               883 TLWIYELDQLREIRFEDGSSPLLEKIEIGECRLESGI--TGIIHLPKLKEIPIRYGSKVA 940
                                                                      |:| : :|: | ||||:|||||:||| vIDGMSTTEEWDQIKP-CFP-NNKRGSRIIVSTKQVEVASLCAGPQNVAPEHKQFSIDQN 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LKPCFLYLSIFPEDFEIKRNRLVGRWIAEGF---VRPKVGMTTKDVGESYFNELINRSMI 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QRSRVGIAG--KIKTCRIHDIIRDITVSISRQENFVLLPMGDGSDL-VQENTRHIAFHGS 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----CIGQFHYDNFSLNHPMKCITNTICLPKVFTPLVSRDDRAKQIAELHMATK 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              870 AGFPTKGNYLCTRHLLH-TYGFNQLDAC-TSLCC--GAATPCIMMD------- 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        707 SCWSESIGVKVPKGIGKIRDLQVLEYVDIRRISSRAIKELGQLSKLRKLGVTTNGSTKEK 766
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                                                                                                                                     DSKKRLLEMIDTNANDGPAKVICVVGMGGLGKTALSRKIFESEEDIRK--NFPCNAWITV 225
                                                                                                                                                                 SQSPHRIELLKDMIRQ----LLGPSSLDQLLQELQGKVVVQVHHLSEYLIEELKERRYFV 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                        340 TLYAFFEKGSQDGDSTEVGSSSTNSTTTASHILVNNKILTRMETTLAAFKEFQLIGREKE 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               400 KSEIIQLVTNGDGCQFEVISVCGMGGLGKTTVVRDVYQSQELRGKFEKCACVTIMRPFNC 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   460 DELLKNLAGQFGYEDVADMVRHLEGKKCLIVLDDLSSTREWDAIIPHFTALETSSRIIVT 519
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                                              -----SYAEDIRNQSAR-NVDEAELVGFS 167
                                                                                                                                                                                                                                                                      222 MCPFNSVEFMRSIIRQFYIDLLQDPVENMDAQVLRGMGMKKENDLVDEFKSYLNDKSYLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----EKCATASL----
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                                                                                                                                                                                                                                                                                                                     VLDDLW1LHDWNWINEIAFPKNNKKGSRIVITTRNVDLA------
                                              EEVSSRNTRYSLVKPISSGTEIDMD-
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Kamihara K.,

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Indels 368; Length 1251;

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| 288 KKC<br>258           | KKCFQKCRKGSRIIVSSTQVEVASLCAGQESQASELKQLSADQTLYAFYDKGSQIIEDSV 347                                                             |
|--------------------------|------------------------------------------------------------------------------------------------------------------------------|
| 348 KPV                  | KPVSISDVAITSTNNHTVAHGEIIDDQSMDADEKKVARKSLTRIRTSVGASEESQLIGRE 407                                                             |
| 258 KW<br>  :<br>408 KBI | KVVVQVHHL                                                                                                                    |
| 267                      | ILVELLRSLABQLHKGSSKKEELLENRVSSKKSLASMEDTELTGQLKRLLEKKSCLIVLD 527                                                             |
| 285 DLI<br> <br>528 DF   | DLWILHDWRWINEIAFPKNNKKGSRIVITTRNVDLAEKCATAS-LVYHLDFLQWNDAITL 343<br>   -  -  -                                               |
| 344 LL<br>               | LLRKTNKNHEDMESNKOMOKMVERIVNKCGRLPLAILTIGAVLATKQVSEWEKFYE 399                                                                 |
| H :: E                   | 400 HLPSELEINPSLEALRRAVTLGYNHLPSHLKPCFLYLSIFPEDFEIKRNRLVGRWIAEGF 459 :::   :                                                 |
| 460 VF                   | 460 VRPKVGMTTKDVGESYFNELINRSMIQRSRVGIAGK-IKTCRIHDIIRDITVSISRQ 515<br>  : :                                                   |
| 516 E                    | ENFVLLPMGDGSDLVQENTRHIAFHGSMSCKTGL-DWSIIRSLAIFGDRPKSLAHA 570                                                                 |
| 571 V                    | VCPDQLRMLRVLDLEDVTFLITQKDFDRIALLCHLKYLSIGYSSSIYSLPRSIGKLQGLQ 630KMRFIRVLDFEG-TRGLEXHHLDQIWKLNHLKFLSLRGCYRIDLLPDLLGNLRQLQ 879 |
| 631 TI<br> <br>880 MI    | 631 TLAMPSTYIAALPSEISKLOCLHTLRCIGOFHYDNFSLANHPMKCITNTICLPKV 684  ::          :        :                                      |
| 685 FT                   | FTPLVSRDDRAKQIAELHMATKSCWSESIGVKVPKGIGKLRDL 727 :                                                                            |
| 728 Q<br>990 H           | 728 QVLEYVDIRRISSRAIKBLGQLSKLRKLGVTINGSTKEKCKILYAAIEKLSSLQSLHVDA 787<br>  :::   ::::   :                                     |
| 788 A<br> <br>1047 A     | AGISDGGTLECLDSISSPPPLLRTLVLDGILEEMPNWIEQLTHLKKIYLLRSKLKE-GKT 846                                                             |
| 847 M<br> <br>  1105 M   | MLILGALPNLMVLHLYRNAYLGEKLVPKTG-ÄFPNLRTLMIYELDQLREIRFEDGSS 902                                                                |
| 903 P                    | PLIEKIEI-GECRLESGITGIIHLPKLKEIPIRYGSKVAGL 942     ::::                                                                       |
| 943                      | GQLEGEVNAHPNRPVL 958<br> : : :: :  : : :<br>VQEARRKGGELKRKIREQLARNPNQPII 1250                                                |
|                          |                                                                                                                              |

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19 Q947C8
10 DEC-2001 (TERMELrel. 19, Leat esquence update)
10 Q1-DEC-2001 (TERMELrel. 25, Leat annotation update)
10 Q1-DEC-2003 (TERMELrel. 25, Leat annotation update)
10 Q1-DEC-2003 (TERMELrel. 25, Leat annotation update)
10 DECT-2003 (TERMELrel. 25, Leat annotation update)
10 DECT-2003 (TERMELrel. 25, Leat annotation update)
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15 DECT-2003 (TERMELrel. 25, Leat annotation update)
16 DECT-2003 (TERMELrel. 25, Leat annotation)
17 DECT-2003 (TERMELrel. 25, Dected 20, Leat annotation)
18 DECT-2003 (TERMEL.)
18 DECT-2003 (TERMELRel. 25, Dected 20, DSKKRLLEMIDTNANDGPAKVICVVGMGGLGKTALSRKIFESBEDIRKN--FPCNAWITV 225 221 339 320 EEVSSRNTRYSLVKPISSGTEIDMD-----SYAEDIRNQSAR-NVDEAELVGFS 167 SOSFHRIELLKDMIRQ----LLGPSSLDQLLQBLQGKVVVQVHHLSBYLIEELKEKRYFV 281 281 KSEIIQLVTNGDGRQFEVISVCGMGGLGKTTVVRDVYQSQELRGKFEKCACVTIMRPFNC 459 DELLKNLAGQFGYEDVADMVRHLEGKKCLIVLDDLSSTREWDAIIPHFTALETSSRIIVT 519 TLYAFFEKGSQDGDSTEVGSSSTNSTTTASHILVNNKILTRMETTLAAFKEFQLIGREKE 399 9 9 KD-ELLKVWAEQIRDLSYDIEDSLDEPKVHIESQTLFRQLVKLRERHRIAIRIHNLKSRV 1 MAETVLSMARSLVGSAISKAASAAADETSLLLGVEKDIWYIKDELKTMQAFLRAAELMKK VLDDLWILHDWNWINEIAFPKNNKKGSRIVITTRNVDLA---------------EKCATASL Gapa Query Match 22.8%; Score 1200; DB 2; Length 1169; Best Local Similarity 28.5%; Pred. No. 1.6e-55; Matches 351; Conservative 201; Mismatches 345; Indels 334; 61 63 120 168 179 226 222 282 282 321 340 400 321 셤 ઠે g ò 셤 ઠે 유 ò 셤 è 요 ઠે 용 ઠે 요 셤 ઠ ઠે

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121 KVEDVSLRNSRYKLLGGPAAASEPSPLTAAELQSTTFDDIEATRVAKQQEKVDLVDLITK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IKTYLPNKHNGSRILVCTPQAEVAICWKNKDGYKVSEIRQEGŚFVTPLYVFYEBVKDSPT 360
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                                                                                                                                                                                                     581;
                                                                                                                                                               Length 1485;
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  Disease_resist.
                   InterPro; IPR001611; LRR.
InterPro; IPR000209; Pept_S8_S53.
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InterPro; IPR000767;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCWSESIGVXVPKGIGKLRDLQVLEYVDIRRISSRAIKELGQLSKLRKLGVTTNGSTKEK 766
  ----VYHLDFLQMNDAITLLLRKTNKNHEDM-ESNKNMQKMVERIVNK 371
                                                                                                                                                                                                                                                                                                                                                                                                                                    CGRLPLAILTIGAVLAT - - KQVSEWEKFYEHL - PSELEINPSLEALRRMVTLGYNHLPSH
                                                                                                     QRSRVGIAG--KIKTCRIHDIIRDITVSISRQENFVLLPMGDGSDL-VQENTRHIAFHGS
                                                                                                                                                                                                                                                                                                                              -----MSCKTGLDWSIIRSLAIFGD-RPKSLAHAVCPDQLRMLRVLDLEDVTFLITQKDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         883 TLWIYELDQLREIRPEDGSSPLLEKIEIGECRLESGI--TGIIHLPKLKEIPIRYGSKVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (japonica cultivar-group).
Sukaryota, Viridiplantea; Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
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Saeaki T., Matsumoto T., Yamamoto K.;
"Oryza ativa nipponbare(GA3) genomic DNA, chromosome 8,
clone:P0666G10.";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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25-OCT-2004 (TEMBLE) 28,
25-OCT-2004 (TEMBLE) 28,
Putative Pi-b procein.
Name=P0666G10.130;
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SEASAÍ T., Mateunco T., Yamamoto K., Sakata K., Baba T., Katayose Y., Mu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H., Hosokawa S., Magukawa M., Arikawa K., Chiden Y., Hayashi M., Okamoto M., Ando T., Anita K., Hamada M., Harada C., Honda M., Ichikawa Y., Idonuma A., Iijima da C., Hibishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M., Ikeno M., Karasawa W., Kategiri S., Kikuta A., Kobayashi N., Kono I., Karasawa W., Kategiri S., Kikuta A., Kobayashi N., Kono I., Machita K., Machara T., Mizuno H., Mizubayashi T., Mukai Y., Makai X., Magasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamira M., Nakashima M., Nakama Y., Nakamichi Y., Nakamira M., Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tguji K., Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tguji K., Anaki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yushawa K., Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
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                                               GKLHHLKYLSLRGSATILNLPSSFGNLLNLETLDIRGTWYTKLPATIGRLQNLKYLHA-G
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                                                                                 SRVGIAGKIKTCRIHDIIRDITVSISRQENFVLLPMGDGSDLVQENTRHIAFHGSMS---
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Similar to Oryza sativa gene for Pib.
Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 21.7%; Score 1144; DB 2; Length 1011; Best Local Similarity 31.2%; Pred. No. 1.3e-52; Aatches 329; Conservative 193; Mismatches 374; Indels 158;
                       1.";
                                                                                                                                                                                                                                                                                                                   PRINTS; PR00364; DISEASERSIST.
PROSITE; PS00053; RIBOSOMAL S8; UNKNOWN 1.
SEQUENCE 1011 AA; 114012 MW; 14EDDBBA31A4835C CRC64;
                          chromosome
                                                                                                                                                            pathogen; IEA
                       rice
                                                                                  Gramens, Q9LJ10; -. Gramens, Q9LJ10; -. GO; GO: 0005524; F: ATP binding; IEA. GO; GO: 0005915; P: apoptosis; IEA. GO; GO: 0042829; P: defense response to pat InterPro; IPR000767; Disease_resist. InterPro; IPR001611; IER. InterPro; IPR001818; NB-ARC. InterPro; IPR006318; Ribosomal_S8.
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Yano M., Jiang J., Gojobori T.;
The genome sequence and structure
Nature 420:312-316(202).
EMBL; AP001073; BAA89580.1; -.
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Pfam; PF00931; NB-ARC;
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SRIVITTRNVDLAEKCA--TASLVYHLDFLQMNDAITLLL---RKTNKNHEDMESNKNMQ 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 881 LRTLWIYELDQLREIRFEDGSSPLLEKIEIGECR-LESGITGIIHLPKLKEIPIRYGSKV 939
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                                                                                                                                                                                                                                                                                                                         ----SGLKASHGVIRNWAKIQSLVHVEIKEHPS-VFQEIALLQNLRKLSVLFYG-IE
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                                                                                                                                                                                                                                                                                                                                                                                                                   480 INRSMIQRSRVGIAGKIKTCRIHDIIRDITVSISRQENFVLLPMGDGSDLV-QENTRHIA
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                                       SRIIVTTRNEDVANTCCCRPQDRIYKIQ--RLSDAASRELFFKRIFGMADAGAPDDDELK
                                                                                                                                         KMVERIVNKCGRLPLAILTIGAVLATK---QVSEWEKFYEHLPSELEINPSLEALRRMVT
                                                                                                                                                                             539 FHGSMSCKTGLDWSIIRSLAIFGDRPKSLAHA----VCPD------QLRMLRVLDLE
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative NBS-LRR type resistance gene.
Name=col1449-H02.21;
Name=col1449-H02.21;
Name=col1449-H02.21;
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
NCBL_TaxID=39947;
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Subnitted (JAN-2002) to the EMBL/GenBank/DDBJ databa
EMBL, AP004648; BAD01287.1;
GO; CO:0005524; F.ATP binding; IEA.
GO; GO:0006515; P:appptosis; IEA.
GO; GO:004829; P:adefense response to pathogen; IEA.
InterPro; IPR000767; Disease_resist.
InterPro; IPR001611; IRR.
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                                                                               807 PLLRTLVLDGILEEMPNWIEQLTHLKKIYLLRSKLKEGKTML-ILGALPNIMVLHLYRNA 865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           YLGEKLVFKTGAPPNLRTLWIYELDQLREIRFEDGSSPLLEKIEIGECRLES-GITGIIH 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YMGRELHFREKLFPRIKQLIVDNMPNLDELSFQ-GGAPELERLTLAVLKEPADGISGIDK 961
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                                                                                                                                                                                                                        DLPSLTKLCVMNCEKGPNKWKPFIVSLNKLSYSLRSLSILHWLNEDAGLEELLD-LDSPP
                                                                                                                                                                                                                                                                                                                                                          844 IFLEKPFLWGKLSMLPPWVSHLGNLVDL-SLRENFLDGKEVIEQLGKLPSLLSLKLYYQS
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                                                                                                                                                                             748 QLSKLRKLGVTTNGSTKEKCKILYAAIEKLS-SLQSLHVDAAGISDGGTLECLDSISSPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (japonica cultivar-group).
Sukaryota, Viridiplantea, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Olywe 10702F05.";
clone:P0702F05.";
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005828; BAD46437.1; -.
SEQUENCE 989 AA; 109590 MW; 09BF11AAD9C3028A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-OCT-2004 (TrEMBLrel. 28, Last sequence update) Similar to NBS-LRR type resistance gene.
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| PRLKEVEF-FGHVIVDSVVESMVAVCKKHPNKP 994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=39947;
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25-OCT-2004
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Pfam; PF00560; LRR 1; 2.
Pfam; PF00931; NB-ĀRC; 1.
PRINTS; PR00934; DISEASERSIST.
SEQUENCE 884 AA; 101271 MW; 3D03F1A1FC00BF3A CRC64;
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Search completed: Pebruary 9, 2005, 08:47:51 Job time : 136.377 secs

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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-930-996A-4

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Gapop 10.0 , Gapext 0.5
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APPLICATION NUMBER: US/08/930,996A
FILING DATE: 09-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05272
FILING DATE: 15-APR-1996
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COMPUTER: IBM PC COMPATIBLE
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                              ; Sequence 8, Application US/08930996A; Patent No. 6100449; GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                  APPLICANT: ESHED, Yuval
APPLICANT: ORI, Macmi
APPLICANT: PARAN, Ilan
APPLICANT: ZAMIR, Daniel
IITLE OP INVENTION: A GENET
IITLE OF INVENTION: LOCUS
IITLE OF INVENTION: SELECT
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409 FDKYVFVTIMRPFILVELLRSLAEQLHKGSSKKEELLENRVSSKKSLASMEDTELTGQLK 468
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                                                                                                DSKKR-----LLEMIDTNANDGPAKVICVVGMGG-LGKTALSRKIFESEEDIRKNF 217
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                          MQAFLRAAELMKKKDELLKVWAEQIRDLSYDIEDSLDEFKVHIESQTLFRQLVKLRERHR 107
                                                                              108 IAIRIHNLKSRVEEVSSRNTRYSLVKPISSGTEIDMDSYAEDIRNOSARNVDEAELVGFS 167
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                                           Gaps
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188; Mismatches 351; Indels 368;
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835 YLLRSKLKE-GKTMLILGALPNLMVLHLYRNAYLGEKLVFK---TG-AFPNLRTLWIYEL
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llarity 29.2%; Pred. No. 3e-75;
Conservative 194; Mismatches 359;
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419 Seventh Street, N.W., Suite 300
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SLVGIDAPKGKLIGRL---LSPEPQRIVVAVVGMGGSCKTTLSANIFKS-QSVRRHFESY 225
                                               AWITVSQSFHRIELLKDMIRQLLGPSSLDQLLQELQGKVVVQVHHLS-----EYLIEELK 275
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                                                                                                                                                          WIAEGFVRPKVGMTTKDVGESYFNELINRSMIQRSRVGIAGKIKTCRIHDIIRDITVSIS 513
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                                                                                            EKRYFVVLDDLWILHDWNWINBIAFPKNNKKGSRIVITTRNVDLAE-KCATASLVYHLDF 334
                                                                                                           WEKFYEHLPSELEINPSLEALRRMVTLGYNHLPSHLKPCFLYLSIFPEDFEIKRNRLVGR 453
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Patent No. 6479731

GENERAL INFORMATION:

APPLICANT: Valent, Barbara S.

APPLICANT: B. I. du Pont de Nemours and Company

TITLE OF INVENTION: A Pi-ta GENE CONFERRING DISEASE RESISTANCE TO F

PILE REPERENCE: BB-1136

CURRENT FILING DATE: 1999-06-21

PRIOR APPLICATION NUMBER: 60/095229

PRIOR APPLICATION NUMBER: 60/095229

PRIOR PILING DATE: 1998-08-04

NUMBER OF SEQ ID NOS: 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GMGGLGKTALSRKIFESE-EDIRKNFPCNAWITVSQSFHRIELLKDMIRQLLGPSSLDQL 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --blestrestrantiv-klpekigglohlotleadaratavl-ldivhtgcl
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                                                                                                                                                                                         Length
                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                      12.2%; Score 641.5; DB 4;
llarity 24.2%; Pred. No. 1.9e-47;
Conservative 168; Mismatches 380;
  97
SOPTWARE: Microsoft Office SEQ ID NO 2 LENGTH: 928 TYPE: PRT
                                                                                      , okganism: Oryza sativa
US-09-336-946B-2
                                                                                                                                                                                Query Match
Best Local Similarity
Matches 257; Conserv
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| Db 764AANEGFGSIKYPMFVCTAPCMTFVEGAMPSVQRL 797  Qy 891 QLREIRFEDGSSPLLEKIEIGERLESGITGIIHLPKLEEIPRYGSKVAGLG 943                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |

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LOCATION: 1..1402
OTHER INFORMATION:
                    NUMBER OF SEQUENCES:
FITLE OF INVENTION:
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STRANDEDNESS:
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US-09-004-838-11
                                                                                                                   COUNTRY:
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                                                                       ||:||| |: : : : | | | |:: | GGVGKTTLATEFYRLHGRRLDAPFDCRAFVRTPRRKPDMTKILTDMLSQL-----RPQH 290
                                                                                                                                                                                                                                                                     TELEPVALACCGYNSEHIIKIDPLGDDVSSQLFFSGVVGQGNBFPGHLTEVSHDMIKKCG 409
                                                                                                                                                                                                                                                                                                                                   409 GLPLAI-TITARHFKSQLLDGMQQMNHIQKSLTTSNLKKNPTLQGMRQVLNLIYNNLPHC 467
                                                                                                                                                                                                                                                                                                                                                                              LKPCFLYLSIPPEDFEIKRNRLVGRWIAEGFVRPKVGMTTKDVGESYFNELINRSMIQRS 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                  547
                                                 YAEDIRNOSAR-----NVDEA----ELVGPSDSKKRLLEMIDTNANDGP-AKVICVVGM 194
                                                                                                                                                                                                                                                TRNVDLAEKCATASLVYHLDFLQMNDAITLLLRKTNKNHEDMESNKNMQKMVERIVNKCG 373
                                                                                                                                                                                                                                                                                                               374 RLPLAILTIGAVLATKOVSEWEKFYEHL----PSELEINPSLEALRRMVTLGYNHLPSH 428
                                                                                                                                                                                                                                                                                                                                                                                                ----GLDWSIIRSLAIFGDRPKSLAHAVCPDQL----RMLRVL-----DLBDVTFLITQK 594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRCIGGFHYDNFSLNHPMKCITNTI--CLPKVFTPLVSRDDRAKQIAELHWATKSCWSES 712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            893 REIRFEDGSSPLLEKIEIGECRLESGITGIIHLPKLKEIPIRYG-----SKVAGLGQL 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            798 -NLRPNANEFK------QYDSKETGLEHLVALABISARIGGTDDDESNKTEVESAL 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             773 AIEKLSSLOSLHVDAAGISDGGTLECLDSISSPPPLLRTLVLDGILEEMPNWIEQLTHLK 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              764 -----AANEG-----FGSLKYFMFV-----CTAPCMTFVEGAMPSVQRL----- 797
                                                                                                                                                                                BLOGKVVVQVHHLSEYLIBELKEKRYFVVLDDLWILHDWNWINEIAFPKNNKKGSRIVIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    528 DVNCKNEVLSCVVHHMVLNFIRCKSIEENFSITLDHSQTTVRHADKVRRLSLHFSNAHDT
                                                                                                                 GGLGKTALSRKIPESE-EDIRKNPPCNAWITVSQSFHRIELLKDMIRQLLGPSSLDQLLQ
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Patent No. 6350933
GENERAL INFORMATION:
APPLICANT: Michelmore, Richard W.
APPLICANT: Shon, Kathy
APPLICANT: Meyers, Blake
TITLE OF INVENTION: Procedures and Materials for
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Best Local Similarity 23.6%; Pred. No. 2.5e-45;
Matches 245; Conservative 178; Mismatches 345; Indels 270;
Conferring Pest Resistance in Plants 140
                                                                                                                                                                                                                                                                                                                                                         PatentIn Release #1.0, Version #1.30
                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,838
FILING DATE: 09-JAN-1998
CLASSIFFICATION NUMBER: US 08/781,734
APPLICATION NUMBER: US 08/781,734
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORWATION:
NAME: BINDATH, GREGOTY P.
REGISTRATION NUMBER: 38,440
REGISTRATION NUMBER: 38,440
REGISTRATION NUMBER: 38,440
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
THE EDUMNE AT TO INFORMATION:
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TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1402 amino acids
                                                                                                                                                                                                                  ZIP: 94111-3834
COMPUTER READABLE FORM:
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| 110 IRIHNLKSRVEEVSS                                              | Qy 132VKPISSGTEIDMDSYAEDIRNQSARNVDEAELVGFSDSKKRLLEMIDTNANDGPAK 187      | QY 188 VICVVGMGGLGKTALSRKIFESEEDIRKNFPCNAWITVSQSFHRIELLKDMIRQLLGFSS 247                   | QY 248 LDQLLQGKVVVQVHHLSEYLJEELKEKRYFVVLDDLWILHDWNWINEIAFPKNNKKG 307 :::   ::   : | QY 308 SRIVITTRNVDLAEKCATASLVYHLDFLQMNDAITLLLRKTNKOHHDDMESNKNMQKMVER 367 | QY 368 IVNKCGRLPLAILTIGAVLATKQ-VSEWEKFYEHLPSELEINPSLEALRRWVTLGYNHLP 426 | QY 427 SHLKPCFLYLSIFPEDFEIKRNRLVGRWIABGFVRPKVGMTTKDVGESYFNELINRSMI- 485                                                              | Qy                                                                                    | QY 531QENTRHIAFHGSMSCKTGLDWSIIRSLAIFGDRPKSLAHAV 571  DD 512 YKMQPFKRVTGDEINYCPYGLYRALLTPVNRQLRDHDNNNLLKRTHSVFSFHLEPLYYVL 571 | QY 572 CPDQLRMLRVLDLEDVTFLITQKDFDRIALLCHLKYLSIGYSSIYSLPRSIGK 625 : :::   :  : | QY         626 LQGLQTLAMPSTYLAALPSEISKLQCLHTLRCIGQFHYDNFSLAHPWKCITNTICLPK 683 | QY 684 VFTPLVSRDDRAKQIABLHMATKSCWSESIGVKVPKGIG-KLRDLQVLEYVDIRRTSSRA 742  : | Qy 743 IKELGQLSKLRKLGVTTNGSTKEKCKILYAAIEKLSSLQSLHVDAAGISDGG 794                                                             | QY 795 -TLECLDSISSPPLLRTLVLDGILEEMPNWIEQLTHLKKIYLLRSKLKEGKTWLLLGAL 853                                                                                   | 854 PNLMVLHLYRNAYLGEKLVFKTGAFPNLRTLWIYELD                                                                  | 782 PNLEVLKLMDDACCGEEWHPIVMGFNRLKLLLIKYSFLKFWKATNDNFPVLERLMIRSCK | Qy         891 QLREIRFEDGSSPLLEKIEIGECRLESGITGIIHLPKLKEIPIRYGSKVAGLGQLEGEVN 950             : | Qy 951 AHPNRPULLMYSDRRYH 967 | Db 889 VRISNPLKESDSDSEEH 905 | RESULT 8 US-09-864-680A-3 ; Sequence 3, Application US/09864680A ; Patent No. 6762285 |
|------------------------------------------------------------------|-------------------------------------------------------------------------|-------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------|--------------------------------------------------------------------------|-------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------|-------------------------------------------------------------------------------|----------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------|-----------------------------------------------------------------------------------------------|------------------------------|------------------------------|---------------------------------------------------------------------------------------|
| 391 VSEWEKFYEHLPSELEINPSLEALRRMVTLGYNHLPSHLKPCFLYLSIFPEDF ::   : | Qy 444 EIKRNELVGRWIABGFV-RPKVGMTTKDVGESYFNELINRSMIQRSRVGIAGKIKTCRI- 501 | QY 502 HDIRDIT SISRQENFVLLPMGDGSDLVQENTRHIA 538     :-     :-   :-     :-     :-       :- | Qy 539 -FHGSMSCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLED 586      : :       : :   | QY 587 VTFLITQKDFDRIALLCHLKYLSIGYSSSIYSLPRSIGKLQGLQTLNMPSTYIAALPSEI 646  | Qy 647 SKLQCLHTLRCIGQFHYDNFSLNHPMKCITNTICLPKVFTPLVSRDDRAKQIABLHMATK 706 | Qy 707 SCWSESIGVKVPKGIGKLRDLQVL-EYVDIRRTSSRAIKELGQLSKLRK-LGVT 758  1027 PXLKNMPLXIGELXXLQTLFXNIGIAITELKNLXNLHGKXCIGGLGKMENAVGCT 1081 | Qy 759 TNGSTKEKCKILYAAIEKLSSLQSLHVDAAGISDGGTLECLDSISS 804 :       : :       :       : | Qy 805 PPPLLRTLVLDGILEEMPNWIEQLTHLKKIYLLRSKLKEGKTMLILGALP 854   : :                                                          | QY 855 NLMVLHLYRNAYLGEKLVFKTGAPPNLRTLMIYELDQLREIRFEDGSSPLLEKIEIGE 912         | Qy 913 CRLESGITGIIHLPRLKE 930<br>  :   :      <br>  Db 1231 CENLVSLGEKKE 1242 | RESULT 7<br>US-09-360-186-3                                                | ; Sequence 3, Application US/09360186<br>; Patent No. 62823343<br>; GENERAL INFORMATION:<br>; APPLICANT: Staskawicz, et al. | ; TITLE OF INVENTION: B\$2 Resistance Gene<br>; FILE REFERENCE: 50687<br>; CURRENT APPLICATION UMBER: US/09/360,186<br>; CURRENT REFING DATE: 1009-07-23 | ; CORKENI FILING DATE: 1393-07-23<br>; EARLIER APPLICATION NUMBER: 60/093,957<br>; NUMBER OF SEO ID NOS: 9 | ; SOFTWARE: Patentin Ver. 2.0<br>; SEQ ID NO 3                   | IENGTH: 905 ; TYPE: PRT ; ORGANISM: Capsicum annuum                                           | 3                            | 6                            | Qy 50 AFLRAABLMKKDBLLKVWABQIRDLSYDIEDSLDEFKVHIESQTLFRQLVKLREBHRIA 109                 |

853 781 890

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842 NLKEIPIEFADIHTLOLIELRECP------PKLGESAARIOKEOEDLG--NNPVD 888
                                                                                                    ------DYKSFRDSGLPNNLVYL 730
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LOCUS OF TOMATO AND USE THEREOF FOR TRANSFORMATION
SELECTIVE BREEDING OF TOMATO AND RELATED PLANTS
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                                                                                                                                                                         854 PNLMVLHLYRNAYLGEK------LVFK-----TGAPPNLRTLWIYELD
                                                            743 IKELGQLSKLRKLGVTTNGSTKEKCKILYAAIEKLSSLQSLHVDAAGISDGG-----
                                                                                                                                             -TLECLDSISSPPPLLRTLVLDGILEEMPNWIEQLTHLKKIYLLRSKLKEGKTMLILGAL
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
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APPLICATION NUMBER: US/08/930,996A
FILING DATE: 09-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05272
FILING DATE: 15-APR. 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 113,373
                                                                                     , Sequence 4, Application US/08930996A
; Patent No. 6100449
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13-APR-1995
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APPLICANT: BSHED, Yuval
APPLICANT: ORI, Naomi
APPLICANT: PARAN, Ilan
APPLICANT: ZAMIR, Daniel
IITLE OF INVENTION: A GENE
TITLE OF INVENTION: LOCUS
TITLE OF INVENTION: SELECT
NUMBER OF SEQUENCES: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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ADDRESSEE: BROWDY AN
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                     560 PYLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 GEMTDFEVEVREVASAAEYTIQLRLTGTVLGENKSQKKKARRRFRQSLQQVAEDMDHIWK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 ESTKIODKGKQVSKESLVHDF-SSSTNDILKVKNNNVGRDDQRKQLLEDL-TRSYSGEPK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VICTVGMGGLGKTALSRKIFESEEDIRKNFPCNAWITVSQSFHRIELLKDMIRQLLGPSS 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        486 --QRSRVGIAGKIKTCRIHDIIRDITVSISRQENFVLLPMGDGSDLV------ 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --VKPISSGTEIDMDSYAEDIRNQSARNVDEAE--LVGFSDSKKRLLEMIDTNANDGPAK 187
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11.6%; Score 609; DB 4; Length 905;
Best Local Similarity 23.8%; Pred. No. 1.4e-44;
Matches 247; Conservative 176; Mismatches 362; Indels 252;
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            APPLICANT: Stackawicz, Brian J
APPLICANT: Stackawicz, Douglas
APPLICANT: Dahlbeck, Douglas
APPLICANT: Tal, Thomas H
TITLE OF INVENTION: BS2 RESISTANCE GENE
FILE REFERENCE: 42250/234021 (5830-4A)
CURRENT PAPLICATION NUMBER: US 09/360,186
PRIOR FLILNG DATE: 2001-05-24
PRIOR FLILNG DATE: 1999-07-23
PRIOR FLILNG DATE: 1999-07-23
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
SERGIH: 905

    TYPE: PRT
    ORGANISM: Capsicum annuum
US-09-864-680A-3

SENERAL INFORMATION:
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AND

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Sequence 2, Application US/08930996A
          Patent No. 6100449
GENERAL INFORMATION:
APPLICANT: FLUHR,
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                                                   APPLICANT:
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LEFEDMTEWKQWHALGIGEFPTLEKLSIINC------PELSLEIPIQFSSLKRF 886
                                                                                             121 INIKOKLEDTIETLKDLQEQIGLL----GLKEYFDSTKLETRTPSTSLIDEPDIFG--- 172
                                                                                                                                              DLW--ILHDWNWINEIAPPKNNKKGSRIVITTRNVDLAEKCATASLVYHLDFLOMNDAIT 342
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                                                  ENKQASNPSVRDWLNELRDAVDSAENLIEEVNYEALRLKVEGOHONFSETSNOOVSDEFF 120
                                                                             -----LKSRVEEVSSRNTRYSLVKPISSGTEIDMDSYAEDIRNQSARNVDEAELVGFSD 168
                                                                                                                                SKKRLLEMIDTNANDGPA----KVICVVGMGGLGKTALSRKIFESEEDIRKNFPCNAWIT 224
                                                                                                                                                                                    VSQSFHRIELLKDMIRQLLGPSSLDQLLQELQGKVVVQVHHLSEYLIEELKEKRYFVVLD 284
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 EIGLAVGGAFLSSALNVLFDRLAPNGDLLNMFRKHKDHVK-LLKKLKMTLRGIQIVLSDA 60
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                           ELLKVWAEQIRDLSYDIEDSLDEFKVHIESQTLFRQLVKLRERHRIAIRIHN-
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RESULT 10 US-08-930-996A-2

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LOCUS OF TOMATO AND USE THEREOF FOR TRANSFORMATION AND
SELECTIVE BREEDING OF TOMATO AND RELATED PLANTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -IHNLKSRVEEVSSRNTRYSLVKPISS-GTEIDMDSYAEDIRNOSARNVDEAELVGFSDS 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 FFLNIKKKLEDTIKK--LEVLEKQIGRLGLKEHFISTKQETRTPSTSLVDDSGIFGRKNE 175
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                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,996A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
11.0%; Score 577.5; DB 3;
Best Local Similarity 23.6%; Pred. No. 1.4e-41;
Matches 241; Conservative 191; Mismatches 371;
                                                                                                                                                                                                                                       ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05272
FILING DATE: 15-APF-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 113,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 13-APR-1995
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1220 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-DEC-1997
                   APPLICANT: ORI, Naomi
APPLICANT: PARAN, Ilan
APPLICANT: ZAMIR, Daniel
TITLE OF INVENTION: A GENET
TITLE OF INVENTION: LOCUS
TITLE OF INVENTION: SELECT
ESHED, Yuval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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S S LGKLEELLRSKLDLIIDLKHQIESVKEGLLCLRSFIDHFSESYDEHDEACGLIA-RVSVM 1017
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10.7%; Score 564; DB 2; Length 1824;
Best Local Similarity 23.6%; Pred. No. 4.4e-40;
Matches 248; Conservative 189; Mismatches 373; Indels 240;
                                                                                                                                      APPLICATION WIMBER: 08/227,360
FILING DATE: April 13, 1994
CLASSIFACATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Alan. E.
REGISTRATION WIMBER: 35,123
REFERENCE/DOCKET NUMBER: 5151-45038
TELECOMMUNICATION INFORMATION:
TELEPRONE: (503) 226-7391
TELEPRONE: (503) 226-7391
TELEPRONE: (503) 226-7391
TELEPRONE: (503) 228-9446
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHRACTERISTICS:
CLASSIPICATION: 800
RIOR APPLICATION DATA:
APPLICATION NUMBER: 08/310,912
FILING DATE: September 22, 1994
CLASSIFICATION: 800
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                                 564 ----PKSLAHAVCPDQLRMLRVLDLEDVTFLITQKD-FDRIALLCHLKYLSIGYSSSIYS 618
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   BHLPSEL-BINPSLEALRRMVTLGYNHLPSHLKPCPLYLSIFPEDFEIKRNRLVGRWIAE 457
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------KIPLHLSRLKSLQVLVGAKFLV 691
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                                                                                                                GPVRPKVGMTTKDVGESYFNELINRSMIQRSRVGIAGKIKTCRIHDIIRDITVSISRQEN
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'Sequence 3, Application US/08680327

'Sequence 3, Application US/08680327

'Patent No. 5859221

'GENERAL INFORMATION:

APPLICANT: Staskawicz, Brian S., Oldroyd, Giles Edwar APPLICANT: Staskawicz, Dobros Title OF INVENTION: COMPOSITIONS AND METHODS FOR PLANTILE OF INVENTION: PATHOGEN RESISTANCE

'ITILE OF INVENTION: PATHOGEN RESISTANCE

'NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Whinston

STREET: One World Trade Center

STREET: 121 S.W. Salmon Street

STREET: Suite 1600
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: Wordberfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/680,3
FILING DATE: July 11, 1996
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COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3.
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1168 NDVLEPSDRN---EKEDGEIADELRRF-----LLTKRFLILIDDVWDYKVWDNLCMCF 1217
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                                                                                1761 ---HLEK---IPSRFEDAVC-LNRV--EVNW----------CNWNVANSAQDI 1794
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                                                                                                                     SSPPPLLRTLVLDGILEEMPNWIEQLTHLKKIYLLRSKLKEGKTMLILGALPNLMVLHLY 862
                                                                                                                                                                                                                        GIIHLPKLKEIPIRYGSKVAGLGQLEGEVNAHPNRPVLLMYSDRRYHDLGAEAEGSSIEV 980
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                589 VSRDDRAKQIAELHMATKSCWSESIGVKVPKGIGKLRDLQVLEYVDIRRTSSRAIKELGQ 748
                                                                 749 LSKLRKLGVTTNGS-----TKEKCKILYAAIEKLSSLOSLHVDAAGISDGGTLECLDSI 802
                                                                                                                                                                      963 RNAYLGEKLVFKTGAFPNLRTLWIYELDQLREIRF--EDGSSPLLEKIEIGECRLESGIT 920
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                                                                                                                                                                                                                                                                                                                                                                                                                      Compositions
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APPLICANT: Stackwicz, B. S. et al.
TITLE OF INVENTION: PRF Protein and Nucleic Acid Sequences:
TITLE OF INVENTION: and Methods for Plant Pathogen Resistance
TITLE OF INVENTION: and Methods for Plant Pathogen Resistance
FILE REFERENCE: 51700
CURRENT FILING DATE: 1990-01-11
EARLIER APPLICATION NUMBER: 08/080,327
EARLIER FILING DATE: 1996-07-11
EARLIER FILING DATE: 1996-07-11
EARLIER FILING DATE: 1994-04-13
EARLIER FILING DATE: 1994-04-13
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
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Patent No. 6245510
GENERAL INFORMATION:
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; ORGANISM: Lycopersicon esculentum
US-09-228-246-2
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                                                                                                                                                                                                                                                       NMOKMVERIVNKCGRLPLAILTIGAVLATKQ--VSEWEKFYEHLPSELEINPSLEALRRM 417
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patent No. 666447

GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: Brommonschenkel, Sergio H.

TITLE OF INVENTION PLANT GENE CONFERRING RESISTANCE TO TOSPOVIRUSES

FILE REFERENCE: 19603/3201

CURRENT APPLICATION NUMBER: US/09/803,286A

CURRENT APPLICATION NUMBER: 60/188,356

PRIOR FILING DATE: 2001-08-31

PRIOR FILING DATE: 2000-03-10

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 1247
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US-09-245-928A-19
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LENGTH: 1206
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                                                                                                      PTPSQPPTFGGLSFLNSLLRKLNEMSTSKSGLGFLMKPLLGNLEKELSSLTSILEKELSS 437
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                                                                                                                                       AA----LLKVWAEQIRDLSYDIEDSLDE
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                                                               Gaps
                                     Query Match
10.7%; Score 561.5; DB 4; Length 1247;
Best Local Similarity 23.5%; Pred. No. 3.9e-40;
Matches 240; Conservative 185; Mismatches 348; Indels 249;
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; ORGANISM: Lycoperation var. US-09-803-286A-2
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:|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|
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Fatent No. 6613962
GENERAL INFORMATION:
FITUE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/245,928A
CURRENT FILING DATE: 1999-02-08
FRICE REFERENCE: 90-03-08
FRICE REPLICATION NUMBER: PCT/EP97/04340
FRICE RILING DATE: 1999-06-08
FRICE REPLICATION NUMBER: EP96401764.4
FRICE FILING DATE: 1996-09
FRICE FILING DATE: 1997-06-16
FRICE RILING DATE: 1997-05-16
FRICE REPRESERVED FRICE RILING DATE: 2.0
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ORGANISM: Artificial Sequence
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KL 1211
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1007 LQF-----PENLDCLTELETLCVG 1039
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                                                                                                                                                                                                                                                                                   790 ISDGGTLECLDSISSPPPLLRTLVLDGILEEMPNW-IEQLTHLKKIYLLRSKLKEGKTWL 848
                    SSIYSLPRSIGKLOGLOTL - NMPSTYIAALPS - - EISKLOCLHTLRCIGOFHYDNFSLN 669
                                                                                              TOVXXLPFSFSNLWNLESLFVSNKGSILVLLPRILDLVKLRVL----SVGACSFFDMDAD 966
                                                                                                                                          670 HPMKCITNTICLPKVFTPLVSRDDRAKQIAELHMATKSCWSESIGVKVPKGIGKLRDLQV 729
                                                                                                                                                                                                               730 LEYVDIRRISSRAIKELGQLSKLRKLGVTINGSIKEKCKILYAAIEKLSSLQSLHVDAAG 789
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RSLAIFGDR-PKSLAHAVCPDQLRMLRVLDLEDVTFLITQKDFDRIALLCHLKYLSIGYS
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TITLE OF INVENTION: RESISTANCE AGAINST NEWATODES AND/OR APHIDS
FILE REFERENCE: 960-35
CURRENT APPLICATION NUMBER: US/09/245,928A
CURRENT FILING DATE: 1999-02-08
FRIOR FILING DATE: 1999-02-08
FRIOR PELLING DATE: 1997-08-08
FRIOR FILING DATE: 1996-08-09
FRIOR FILING DATE: 1996-08-09
FRIOR FILING DATE: 1997-08-16
FRIOR FILING DATE: 1996-08-09
FRIOR FILING DATE: 1996-08-16
FRIOR FILING DATE: 1997-05-16
SEQ ID NOS: 19
SOFWARE: Patentin Ver. 2.0
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Matches 239; Conservative 173; Mismatches 365; Indels 174;
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ORGANISM: Mi resistance gene deduced amino acid
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Patent No. 6613962
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US-09-245-928A-17
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US-09-245-928A-17
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1044 LOF-----FEKESWDYSTECHW-----FPKLDCLTELETLCVG 1076
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                                                                                --TKQVSEWEKFYEHLPSELEINPSLEALRRMVTLGYNHLPSHLKPCFLYLSIFPEDFEI 445
                                                                                                                                       772 TIYLLIVYLGAEGEVEKTEMKGIEEVVKIYMDDLISSSLV--ICFNEIGDILNFQIHDLV 829
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327
                           602 RKQLFGKRYLIVLDDVW---DTTTLDELTRPPBAKKGSRIILTTREKEVALHGKLNTDP 658
                                                                                                                                                                                    KRNRLVGRWIAEGFVRPKVGMTTKDVGESYFNELINRSMIQRSRVGIAGKIKTCRIHDII 505
                                                                                                                                                                                                                                                                                                            555 RSLAIFGDR-PKSLAHAVCPDQLRMLRVLDLEDVTFLITQKDFDRIALLCHLKYLSIGYS 613
                                                                                                                                                                                                                                               RDITVSISRQEN-FVLLPMGDGSDLV-----QENTRHIAFHGSM--SCKTGLDWSII 554
                                                                                                                                                                                                                                                                            830 HDFCLIKARKENLFDRIRSSAPSDLLPROITIDYDEREEHFGLNFVMFDSNKKRHSGKHL 889
IEELKEKRYFVVLDDLWILHDWNWINEIAFP-KNNKKGSRIVITTRNVDLA--EKCATAS
                                                           LVYHLDFLQMNDAITLLLRKTNKNHEDMESNKNMQKMVERIVNKCGRLPLAILTIGAVLA
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Search completed: February 9, 2005, 08:56:16 Job time : 36.2998 secs

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Sequence 89, Appl
Sequence 139799,
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Copyright (c) 1993 - 2005 Compugen Ltd
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APPLICANT: Wang, Guo-liang
APPLICANT: Wang, Guo-liang
APPLICANT: Wang, Guo-liang
APPLICANT: Wang, Guo-liang
APPLICANT: As Guifu
TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pla
TILE REFERENCE: 22727/04108
CURRENT APPLICATION NUMBER: US/10/352,179
CURRENT FILING DATE: 2003-01-27
PRIOR APPLICATION NUMBER: 60/352,106
NUMBER OF SEQ ID NOS: 97
SOFTWARE: Patentin Version 3.1
SEQ ID NOS: 97
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RESULT 2
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; Publication No. US20040006788A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Guo-liang
; APPLICANT: Liu, Guifu

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TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance PILE REFERENCE: 22727/04108
CURRENT APPLICATION NUMBER: US/10/352,179
CURRENT FILING DATE: 2003-01-27
PRIOR APPLICATION NUMBER: 60/352,106
PRIOR FILING DATE: 2002-01-25
NUMBER OF SEQ ID NOS: 97
SOFTWARE: Patentin version 3.1
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Best Local Similarity 95.5
Matches 976; Conservative
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US-10-352-179-89
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APPLICANT: Kovalic, David K. APPLICANT: Kovalic, David K. APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua APPLICANT: Zhou, Yihua APPLICANT: Cao, Yongwei APPLICANT: Wu, Wei APPLICANT: Wu, Wei APPLICANT: Buckharov, Andrey A. APPLICANT: Buckharov, Andrey A. APPLICANT: Li, Ping TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement CURRENT APPLICATION NUMBER: US/10/437,953

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966
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69.6%; Score 3664.5; DB 16; Lengt
Best Local Similarity 73.9%; Pred. No. 5e-266;
Matches 733; Conservative 76; Mismatches 122; Indels
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US-10-437-963-104966
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, Publication No. US20040123343A1
, GENERAL INFORMATION:
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ORGANISM: Oryza sativa
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Each, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Buckharcv, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-65-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 139799
                                                                                                                                                                 961 YSDRRYHDLGAEAEGSSIEVQTADPVPDAEGSVTVAVEATDPLPEQEGESSOSOVITLTT 1020
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US-10-437-963-139799
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ORGANISM: Oryza sativa
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                      LLCHLKYLSIG--YSSSIYSLPRSIGKLQGLQTLNMPSTYIAALPSBISKLQCLHTLRCI
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APPLICANT: Boukharov, Andrey A.
APPLICANT: Brada
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: A. Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53221)
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 143499
LENGTH: 974
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Best Local Similarity 62.9%; Pred. No. 3e-221;
Matches 611; Conservative 139; Mismatches 218; Indels
                                                                                                                                                                                                                            OTHER INFORMATION: Clone ID: PAT_MRT4530_44401C.1.pep
Wu, Wei
Boukharov, 1
                                                                                                                                                                                           ORGANISM: Oryza sativa
FEATURE:
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; Sequence 143499, Application US/10437963 ; Publication No. US20040123343A1 ; GENERAL INFORMATION:

RESULT 5 US-10-437-963-143499

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APPLICANT: La ROSA, Thomas APPLICANT: Kovalic, David APPLICANT: Zhou, Yihua APPLICANT: Cao, Yongwei

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Sequence 141086, Application US/10437963

Sequence 141086, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Cao, Yongwei

APPLICANT: Cao, Yongwei

APPLICANT: Barbazuk, Brad

APPLICANT: Barbazuk, Brad

APPLICANT: Barbazuk, Brad

APPLICANT: Barbazuk, Brad

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21 (53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT APPLICATION NUMBER: US/10/437,963

LENGREN OF SEQ ID NOS: 204966

SEQ ID NO 141086

LENGTH: B62
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                                                    OPHYDNPS-LNHPMKCITNTICLPKVFTPLVSRDDRAKQIAELHMATKSCWSESIGVKVP
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                                   INRSMIQRSRVGIAGKIKTCRIHDIIRDITVSISRQENPVLLPMGDGSDLVQENTRHIAF
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US-10-437-963-141086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 52.6%; Score 2769; DB 16; Best Local Similarity 57.8%; Pred. No. 7.9e-199; Matches 567; Conservative 122; Mismatches 166;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Mang, Gao-liang
APPLICANT: Liu, Guifu
TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in FILE REFERENCE: 22727/04108
CURRENT PILING DATE: 2003-01-27
PRIOR APPLICATION NUMBER: 60/352,106
PRIOR PLIING DATE: 2003-01-27
PRIOR PLIING DATE: 2002-01-25
PRIOR FILING DATE: 2002-01-25
SOFTWARE: Patentin version 3.1
SEQ ID NOS: 97
SEQ ID NOS: 97
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                LOSLHVDAAGISDGGTLECLDSISSPPPLLRTLVLDGILEEMPNWIEQLTHLKKIYLLRS
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962 MAEDRSHHDLG 972
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; ORGANISM: Oryza minuta
US-10-352-179-85
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                                                                                            NANDGPAKVICVVGMGGLGKTALSRKIFESEEDIRKNFPCNAWITVSQSFHRIELLKDMI 239
                                                                                                       ---NNNKGSWVIVTTRDVGLAKECTSELLIYQLKPLEISYAKELLLRKANKTTEDIESDK 334
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RESULT 8
US-10-352-179-87
US-10-352-179-87
; Sequence 87, Application US/10352179
; Publication No. US20040006788A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Guo-liang
; APPLICANT: Liu, Guifu

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TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance: CURRENT APPLICATION NUMBER: US/10/352,179
CURRENT FILING DATE: 2003-01-27
PRIOR APPLICATION NUMBER: 60/352,106
PRIOR PLING DATE: 2002-01-25
NUMBER OF SEQ ID NOS: 97
SOFTWARE: Patentin Version 3.1
SEQ ID NO 87
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ORGANISM: Oryza minuta
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APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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APPLICANT: Wu, Wei
APPLICANT: Bucharov, Andrey A.
APPLICANT: Barbazuk, Brad
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118 VTLGYNHLPSHLKPCFLYLSIFPEDFEIKRNRLVGRWIAEGFVRPKVGMTTKDVGESYFN
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Gao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
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; Sequence 110261, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
    APPLICANT: La Rosa, Thomas J.
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    APPLICANT: Cao, Yongwei
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    APPLICANT: Brabauk, Brad
    APPLICANT: Brabauk, Brad
    APPLICANT: Li, Fing
    TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
    TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
    TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
    TURRENT APPLICATION NUMBER: US/10/437,963
    CURRENT FILING DATE: 2003-65-14
    NUMBER OF SEQ ID NOS: 204966
    SEQ ID NO 110261

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                                                                                  ----- VLIIRNQKQLKEV 875
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                           LLRSKIKEGKTMLILGALPNLMVLHLYRNAYLGEKLVPKTGAFPNLRTLWIYBLDQLREI
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US-10-437-963-110261
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936 PMLRLFGERSRHDLG 950
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                                                                                                            NAWITVSQSFHRIELLKDMIRQLLGPSSLDQLLQELQGKVVVQVHHLSEYLIEELKEKRY 279
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                                                              100 VKLRERHRIAIRIHNLKSRVEEVSSRNTRYSLVKPISSGTEIDMDSYAEDIRNQSARNVD 159
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                                    690 SRDDRAKQIAELHMATKSCWSESIGVKVPKGIGKLRDLQVLEYVDIRRTSSRAIKELGQL
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                           40 YIKDELKTMQAFLRAAELMKKKDELLKVWAEQIRDLSYDIEDSLDEFKVHIESQTLFRQL
          Gaps
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EISLRWNCEVARLGQLLEEVKANPNRPVLLLYNDPSKHDLGDTQEGSG----
Best Local Similarity 52.8%; Pred. No. 3.1e-177;
Matches 520; Conservative 165; Mismatches 262; Indels
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                                                                                 for Conferring Disease
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                                                                                                                                                                                                                                                                                                                     Length 1054;
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44.9%; Score 2367; DB 15;
Best Local Similarity 50.3%; Pred. No. 1.8e-168;
Matches 516; Conservative 149; Mismatches 266;
                                         APPLICANT: Wang, Guo-liang
APPLICANT: Liu, Guifu
APPLICANT: Liu, Guifu
TITLE OF INVENTION: Procedures and Materials for
FILE REFERENCE: 22727/04108
CURRENT APPLICATION NUMBER: US/10/352,179
CURRENT APPLICATION NUMBER: 06/352,106
PRIOR APPLICATION NUMBER: 60/352,106
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2002-01-25
SOFTWARE: Patentin version 3.1
SEQ ID NO 91
Sequence 91, Application US/10352179
Publication No. US20040006788A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Oryza minuta
US-10-352-179-91
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Buckharco, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
      235
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                                                                                                                                                                                                                                                                                                                                YHLDFLQMNDAITLLLRKTNKNHEDMESNKNMQKMVERIVNKCGRLPLAILTIGAVLATK 389
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                                                                      214 RKNFPCNAWITVSQSFHRIBLLKDMIRQLLGPSSLDQLLQBLQGKVVVQVHHLSBYLIBB
                                                                                                          LVGRWIAEGFVRPKVGMTTKDVGESYFNELINRSMIQRSRVGIAGKIKTCRIHDIIRDIT
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; Publication No. US20040123343A1
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; ORGANISM: Oryza minuta
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                                                                                                                                                                                                                                                                                                                                                                                   287 WILHDWNWINEIAFPKNNKKGSRIVITTRNVDLAEKCATASL-----VYHLD----- 333
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                                                                                                                                                                                             MQAFIRAAELAKKKOBILKVWAEQIRDLSYDIEDSLDEFKVHIESQTLFRQLVKIRERHR
                                                                                                                                                                                                                     1 MOAFLRAAEVMKKKDELLK-----LVKLRERHR
                                                                                                                                                                                                                                            IAIRIHNLKSRVEEVSSRNTRYSLVKPISSGTEIDMDSYAEDIRNQSARNVDEAELVGFS
                                                                                                                                                                                                                                                         29 IAIRIHNLKSRVEEVSSRNTRYNLVEPISSGTEDDMDSYAEDIRNQSARNVDEAELVGFS
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for Plant Improvement
                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT4530_74999C.1.pep
US-10-437-963-177336
 TITLE OF INVENTION: Plants and Uses Thereof
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          FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 177336
LENGTH: 812
                                                                               TYPE: PRT
ORGANISM: Oryza sativa
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Sequence 55, Application US/10352179;
Publication No. US20040006788A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pla
TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pla
FILE REPERENCE: 22727/04108
CURRENT APPLICATION NUMBER: 08/10/352,179
CURRENT FILING DATE: 2003-01-27
FRIOR APPLICATION NUMBER: 60/352,106
FRIOR FILING DATE: 2002-01-25
NUMBER OF SEQ ID NOS: 97
SOFTWARE: Patentin version 3.1
SEQ ID NO 95
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                        LDOLREIRFEDGSSPLLEKIEIGECRLESGITGIIHLPKLKEIPIRYGSKVAGLGQLEGE
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26.3%; Score 1384; DB 15
Best Local Similarity 51.6%; Pred. No. 3.5e-95;
Matches 281; Conservative 73; Mismatches 93
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748

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749 LSKLRKLGVTTNGSTKEKCKILYAAIEKLSSLQSLHVDAAGISDGGTLECLDSISSPPPL 808
                                                                                                                                                                                                                                                             809 LRTLVLDGILBEMPNWIEQLTHLKKIYLLRSKLKEGKTMLILGALPNLMVLHLYRNAYLG 868
                                                                                                                                                                                                                                                                                                                       VLLPMGDGSDLVQENTRHIAF----HGSMSCKTGLDWSIIRSLAIFGDRPKSLAHAVCPD 574
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                 635 PSTYIAALPSEISKLOCLHTLRCIGOFHYD-----NFSLNHPMKCITNTICLPKVFTPL
                                                          QLRWLRVLDLEDVTFLITQKDPDRIALLCHLKYLSIGYSSSIYSLPRSIGKLQGLQTLNM
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                                                                                                             Sequence 197236, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Bunkharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TILE REFERENCE: 38-21 (53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 197236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT4530_93011C.1.pep
US-10-437-963-197236
                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Oryza sativa
            GSMSC 545
                                  GSKYC 447
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Sasaki,T., Matsumoto,T. and Katayose,Y.

Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC
clone:P0649C11

L Published Only in Database (2002)

2 (bases 1 to 138870)

Sasaki,T., Matsumoto,T. and Katayose,Y.

Direct Submission

Submitted (21-AUG-2002) Takuji Sasaki, National Institute of
Agrobiological Science, Rice Genome Research Program; Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Pax:81-298-38-7468)

On Apr 8, 2004 this sequence version replaced gi:22415844.

The orientation of the sequence is from SP6 to T7 of the PAC clone.
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chromosome 6,
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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PAC clone:P0649C11, complete sequence.
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| 118   TACTIGITAGACATGGTGTGAATGGTGGGCCCTGTTGTAGGTATGTGGCA   5127   56088   TACTIGITAGACATGGTGGTGAATGGTGGTGAATGGTGGTGTAGTGGTGCTAGTGTGTGT                                         | 958 GAGAAATTCTATGAACATCTTCCTTCAGAACTAGAATAAACCCAAGGCTGGAAGCTTTG 1017 56908 GAGAAATTCTATGAACACCTTCCTTCAGAACTAGAAATAAACCCAAGGCTGGAAGCTTTTG 56967 1018 AGGAGAATGGTGACCCTTCCTTCAGAACTACCATCCCATCTGAAACCTGGAAGCTTTTTG 1077 56968 AGGAGAATGGTGACCCTAGGGTTACAACCCTACCATCCCATCTGAAACCATGCTTTTTTG 1077 1078 TATCTAAGTATCTTTCCTGAGGATTTTGAAATCAAAAGGAATCGTCTAGTAGGTAG |

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The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, M., Yazaki, T., Inlikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shimiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosski, T., Kodama, T., Masuda, H., Kobasahi, Y., Yokomizo, S., Niikura, J., Narikawa, R., Sugiyama, A., Mazuno, K., Yokomizo, S., Niikura, J., Kawai, T., Kawamata, M., Yoshimura, A., Miura, J., Kawai, J., Carninci, P., Adachi, J., Alazwa, K., Rikki, Y., Itoh, M., Kawai, J., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Shibata, K., Shinagawa, A., Shiraki, T., Sohino, M. and Hayashizaki, Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
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2 Journal J. Alzawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashida, Y., Ifada, Y., Ifada, K., Hiramoto, K., Hiramoto, K., Hiramoto, K., Hiramoto, K., Hiramoto, K., Hiramoto, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kalana, T., Kojima, K., Kojima, Y., Kishikawa-Hirozane, T., Kishikawa-Hirozane, T., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Koya, S., Kurihara, C., Kurosane, T., Muura, J., Miyazaki, A., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Masuda, H., Matsubara, K., Murata, T., Mibhi, K., Nomura, K., Namiki, T., Namiki, T., Namiki, T., Namiki, T., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Satoh, H., Sasaki, D., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K
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URL: http://cdnaol.dna.affrc.go.jp/cDNA/
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Mizuno,K., Narikawa,R., Niihura,J., Oka,M., Kyu,R., Sugano,S.,
Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S.,
Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S.,
Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Kie,Q., Yokomizo,S.,
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Itoh,M., Kagawa,J., Kanagawa,S., Katoh,H., Kawai,J.,
Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N., Direct Submission
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AKO67966 3890 bp mRNA linear PLN 24-JUL-2003 Oryza sativa (japonica cultivar-group) cDNA clone:J013122117, full insert sequence.

AK067966

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REPERENCE

LOCUS DEFINITION

RESULT 2 AK067966

AK067966.1 GI:32977984
FLI\_CDNA; CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

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Ota,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takatu-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K., Yasunishi,A. and Hayashizaki,Y.
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mol type="mkNa"
/cultivar="Nipponbare"
/db xref="taxon:39947"
/clone="1013122117"
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Direct Submission

Submitted (28-NOV-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 30-8602, Japan
(E-mail:tsasaki@mias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7468)
NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                         /organism="Oryza sativa
/mol_type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /chromosome="6"
/clone="OSJNBb0026L12"
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Best Local Similarity 73.5%;
Matches 1857; Conservative
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OSJNBD0026L12, *** SEQUENCING IN PROGRESS ***.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGGTATCATTCACCTTCCAAGGCTCAAGGAGTTTCAGTTGAATACAAAGGTAAAGTGG 3005
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HTG; HTGS PHASE2.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTGCTTCTGCGGCTGCGCACACCTCGCTGTTCCAAGAGGGGGTGCTGACATAAGG 3298
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                                                                                                               ATTCTGTTTCATCGCCTCCTCCCCCTATTGAGGACACTCAGGTTGAATGGAAGTCTTGAAG
        TCCAATATCTCTATGTGAATGCTGCAGGAATCTCAGATGGTGGAACACTTGAGTGCCTAG
                          TACAATCTCTCCATATGGATGCTGTGGGATGCACAGGTATTGGAACACTTGAGTGCCTAG
                                                                                                                                                                        AGATGCCTAACTGGATTGAGCAGCTCACCTGAAGAAGATCTACTTATTGAGGAGCA
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Oryza sativa nipponbare(Gh3) genomic DNA,
clone.OSJNBb0026L12
bublished Only in Database (2002)
2 (bases 1 to 122193)
Sasaki,T., Matsumoto,T. and Katayose,Y.
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TITLE

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Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,
Ohteuki, K., Shishiki, T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group: Otomo, Y., Murakami, K.,
Idda, Y., Sugano, S., Fulimura, T., Suzuki, Y., Tsunoda, Y.,
Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, O., Lu, M.,
Narikawa, R., Sudiyama, A., Mizuno, K., Yokomizo, S., Niikura, J.,
Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Yoshimura, A., Miura, J.,
Kawai, J., Carninci, P., Adachi, J., Alzawa, K., RIKEN:,
Kawai, J., Carninci, P., Adachi, J., Alzawa, K., RIKEN:,
Kayawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y.,
Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Yoshino, M. and Hayashizaki, Y.,
Collection, mapping, and annotation of over 28,000 cDNA clones from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Bujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, J., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kobayashi, M., Kodama, T., Kishikawa, Hirozana, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Kodaa, T., Kurosaki, T., Muncach, T., Murata, M., Nagata, T., Miura, J., Miyazaki, A., Mizuno, K., Murata, M., Nagata, T., Mahama, Y., Nomura, K., Numasaki, R., Murata, M., Naiki, T., Narikawa, R., Niikura, J., Nishi, K., Nomura, K., Numasaki, R., Otomo, Y., Ryu, R., Saitoh, H., Satoh, K., Sakai, C., Sakai, C., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Shiraki, T., Shishiki, T., Tagami, M., Tagami, M., Tayaka, T., Tagami, M., Yanada, T., Tanaka, T., Tayaki, K., Yanaka, T., Tomaru, A., Taya, T., Yanada, Y., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yohomizo, S., and Yoshimura, A.
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NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kibhimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T.,
Yamamcto,M. and Nakahama,Y.
FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y.,
FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y.,
Ryimura,T., Ikeda,R., Ishibiki,J., Kawamata,M.,
Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M.,
Kobayashi,M., Sugano,S., Sugiyama,A., Matsubara,K. and Murakami,K.
Genome Exploration Research Group in Riken: Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi,J., Alzawa,K.,
Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T.,
Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K.,
Hiraoka,T., Hori,F., Iida,J., Inamura,K., Imotani,K., Ishii,Y.,
Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J.,
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Submitted (31-JAN-2003) Shoshi Kikuchi, National Institute of
Submitted (31-JAN-2003) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 32K full-length cDNA clones from japonica
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AUTHORS
TITLE
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TITLE

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Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Ota, Y., Saltoh, H., Sakai, C., Sakai, K., Shibata, K., Saktoh, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawi, T., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.
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0; Mismatches 733; Indels 12; Gaps
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="hipponbare"
/db_xref="taxon.39947"
/clone="J023131G18"
                                                                                                                                                                                                                                                                                                                                                                 Length 3231;
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Best Local Similarity 70.1
Matches 1747; Conservative
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| 2057 GCTCGACAAAGGAAAATGTAAGATACTTGTGCAGCCATTGAGAGGTCTCTTCCCTC 2116                                                                                                                             | HUUSO7094 HUUSO7094 HUUSO7094 HUUSO7094 HUUSO7094 HUUSO7094 HUUSO7094 HUUSO7094 HUUSO7094 HUUSO7094 HUUSO7094 HUUSO7094 HUUSO7094 HUGdeum vulgare mRNA for NBS-LRR disease resistance protein ACCESSION MS-LRR disease resistance protein homologue; rga S-9202 gene. MJSO7094.1 GI:2855898 HOrdeum vulgare Hordeum vulgare ONGANISM BELARAYOLA; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum. REFERENCE AUTHORS Madsen,L.H., Collins,N.C., Rakwalska,M., Backes,G., Sandal,N., Krusell,L., Jensen,J., Waterman,E.H., Jahoor,A., Pryor,A.J., Langridge,P., Schulze-Lefert,P. and Stougaard,J. Langridge,P., Schulze-Lefert,P. and Stougaard,J. Langridge,P., Schulze-Lefert,P. and Stougaard,J. Langridge,P., Genomics 269 (1), 150-161 (2003) MEDLINE DIDRED 1271563 REFERENCE AUTHORS Madsen,L.H. TITLE Madsen,L.H. TITLE Madsen,L.H. Biology, Aarhus University, Gustav Wieds Vej 10, DK-8000 C, DENMARK FEATURES |
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| 04   AGA-ACIRGAANTAACCCAAGCCTGAAGCTTTGAGGAGATGGTGACCTTAGTTACA 1042     1257   AGAGGCTTGAGAGCCTTGAAGCCTTGAGGAGATGGTGACCTTAGCTTACA 1316     1043   ACCACCTACCATCCCATCTGAAGCCTTTTGATTTTGTTTTCTTTC | 1640                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |

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AACTAGAAATAAACCCAAGCCTGGAAGCTTTGAGGAGAATGGTGACCCTAGGTTACAACC 1045
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                              CTTCAGATTCACTCATCTACCACCTCAAGCACCTGCAAATAGAGGATGCCACAAATTGC 1094
                                                                                                                                                      AAATCAAAAGGAATCGTCTAGTAGGTAGATGGATAGCAGAAGGGTTTGTTAGACCAAAGG
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// LTains lation="WARTYOSMARSMIGGAISMAASAATEMSILIGVRKDIWFIKDE
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64.8%; Pred. No. 1.8e-262;
ive 0; Mismatches 847; Indels 33;
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                                                                                                                                                                                   /protein_id="CAD45030.1"
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                          /mol_type="mRNA"
/cultivar="Regatta"
/db_xref="taxon:4513"
                                                                                               /gene="rga S-9202"
58. .3112
                                                                                                                                   'gene="rga S-9202"
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/product="NBS-LRR
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DEFINITION Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 6,
ACCESSION
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KEYWGRDS
HTG:
Oryza sativa (japonica cultivar-group)
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                                    Published Only in Database (2001)
2 (bases 1 to 14736)
Sasaki,T., Matsumoto,T. and Yamamoto,K.
Direct Submission
Submitted (04-APR-2001) Takuji Sasaki, National Institute of
Agrobiological Resources, Rice Genome Research Program; Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:181-298-38-7441, Fax:81-298-38-7468)
The orientation of the sequence is from Mi3rev to -21M13 of the BAclone.
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Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA,
clone:OSJNBa0007020
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64.5%; Pred. No. 3.3e-248;
tive 0; Mismatches 859;
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/organism=Oryza sativa (.organism=Oryza satova (.ultivar="Nipponbare" db. xref="taxon:39947" /chromosome="6" /clone="0sJNBa0007020"
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Ishikwa,M., Yanada.H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahadi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T.,
Yamamoco,M. and Nakahama,Y.
FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y.,
FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y.,
Robayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M.,
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Ryu,R., Sugano,S., Sugiyama,A., Narikawa,R., Niikura,Y., Ueda,M.,
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Hiraoka,T., Hori,P., Iida,J., Ilmamura,K. Imotani,K., Ishii,Y.,
Itoh,M., Kagawa,I., Kanagawa,S., Katch,H., Kowda,M.,
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Submitted (31-JAN-2003) Shoshi Kikuchi, National Institute of
Submitted (31-JAN-2003) Shoshi Kikuchi, National Institute of
Saprobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (B-mail:skikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 32K full-length cDNA clones from japonica
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                              Osato, N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                     Score 986; DB 8; Length 4326;
Pred. No. 5.2e-248;
0; Mismatches 860; Indels 54; Gaps
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osa ota,Y., Saitoh,H., Sakai,C., Sakai, K., Sakai, K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,A., Tagawa,A., Takahashi,P., Tagawa,A., Takahashi,P., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K., Yasunishi,A. and Hayashizaki,Y.
                                                                                                                                                                                                                                           /organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/mol type="mRNA"
/db.trel="unpponbare"
/db.xrel="xraom:39947"
/clone="J013103X24"
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Best Local Similarity 64.4'
Matches 1656; Conservative
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| PROPOGSDRGSYLETEGIENDATTRHLVEMLWAMDESPAETVLAAODREDRNRCKICK LEDKVDRLEKEIAALKGEAPPOKARIRLTARRKRALFVPRYOLAPKVRVVEKEVAPAD TPVIIISSDEGERSKRANHSKLEWVATODDEDEPNEPSINLLCSEELE"  complement (2506728064) /note="5" LTR" /note="5" LTR" /note="Similar to 22 kDa kafirin cluster; Ty3-Gypsy type (AF061282)" /codon start=1 /proteIn_id="BAA90794.1" /db xref="0" 1693859" /translation="MKKRLITARPVLTLPDIRKDFEIFYDASRQGLGCVLMQERKVVAY ASRQLRPHEVNYPTHDLELAAVVHALKIWRHYLIGNRCEVYTDHKSLKYIFTQTELNM                                                                                                                                                                                                                                                                                              | RQRRWILELIKOYDICHIYHPGRANVVADALSHKAYCNIRPQBALCKELERIKLIT VVQSDDQGTVWCGPRICVPAKKELRDLILKEAHESAYSIHPGSTKMYQDIKAYFWWAG MKRUDVAEYVALCDICQRVKAEHQRPAGLIQPLPIPSKKWEBIGMPFITDLPRTPEGYD SIWVIVDRLTKSAHFVPVKTTFDGKKLAELYMTHVVCRFGCPKKIVSDRGTQFTSRFW KQLHBALGTDLMPSTRATHPHTPGGYTSKVNQILEDMLAFACLDFBGFWRCLPPFRFW QSRQKNYADNRRPNEAPRGTSRVYGTSRVQILEDMLAFACLDFBGFWRCLPFRFY QSRQKNYADNRRPDLEPEKGDHYYLRVSPLRGMRRFCMSSKLAPRYIGPYLITBRELKTA BRQTRRKTIKFYKVQMSNHSEDEATWBREDLLRAEFPELLP" LTR COMDIEMBELT IKFYKVQMSNHSEDEATWBREDLLRAEFPELLP" |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | EDEGGTVWLGERICYEDNKOLKDAILKEAHDTLYSIHPGSTKGYODLKERFWWASMKR EIABTVAVCOVCORVKAEHQKPGGLLOPLKIPENKREIGHDFTTGLPRTSSGHDSIW VIVDBLIKVOAHTPYVKTYSGSRLABLYWARITOTGHOPTTGLPRTSSGHDSIW VIVDBLIKVAHTPYCOTGGTERNYGILEDMLRAGALDFGGSWDRYLPYBERSYNNS YQASLOMAFYBALYGRKCRTPLLMOGTGEROVFGTDILREABEKKVKVIGERLRVAGSR HKSYADNRHRDLSFERGOTVTRENANIEOTLERGENKVKVIGERLRVAGSR HKSYADNRHRDLSFERGOTVTRAVTRYPELGGYHRFHTRGKLAPRRVGFYKIASRGGVAY GLELPOSLAGVHNWFHVSQLKKCLRVPTERANIEOTEVGEDLTVYRKPIRIETRRR TRNRVIRFCKVQWSNHSEESTWBREDBLKSAHPHLFASSESRGRDSV" complement (189728 39519) internal region (AB014741)" /codon start=1 /protein id="BAA90796.1" /db_xref="G" (2691861" / protein id="BAA90796.1" /db_xref="G" (2691861" / krnvtvtlnNSEDIPSVWFERGEROVBELTMSFYRH | PROPOGESTIGNING THE TEATER TO THE TRANSMENT TO THE TOWN THE TEATER THE TEATER THE TEATER THE TEATER THE TEATER THE TEATER THE TEATER THE TEATER THE TEATER THE TEATER THE TEATER THE TEATER THE COMPLEMENT (40024 · .43033)  LTR                                                    | gene. hypothetical protein" /codon_start=1 /protein_id="BAA90797.1" /db_xref="G1:6983862" /tranalation="MG1SSYRRKYKSMPPSPSRAKFPLLPSPACDALTPDLSRRSGGK PNKQKRRTPGQVGLRFCSSSYLWSDSSPPSSSSPISHRPIGGARSKRPPATMIYRNWS LLSSTVVIWGGYATAGLAGFIPLFGGKEKFQNYLCREGERLRQQDRAAMGKN" COMplement(join(5482057727,5860858723)) |
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| Tel:81-298-38-7441, Fax:81-298-38-7468) The orientation of the sequence is from SP6 to T7 of the PAC clone. Genes were predicted from the integrated results of the following:GENSCAN1.0, BLASTN2.0, BLASTN2.0 as well as SplicePredictor (October1998 version). The genomic sequence was searched against the non-redundant database NRP(PIK,SMISSPROT, GENPEPT, PDB) from MAFF DNAbank and the cDNA sequence database at RGP. Protein similarities of the cording regions were searched against NRP with BLASTD2.0. ESTS represent the identified cDNA sequences using BLASTN2.0 with the corresponding DDBJ accession no. and RGP clone ID.  Detailed information on assemble quality together with annotation of this entry at http://www.dna.affrc.go.jp:82/genomicdata/GenomeFi | nished.html.  Location/Qualifiers  Locations agains a sativa (japonica cultivar-group)"  /organism="Cryza sativa (japonica cultivar-group)"  /onlityar="Nipponbare"  /db.xref="taxon:39947"  /chromosome="6"  /clone="00425F02"  36. 254                                                                                                                                                                                                                                                                                 | /note="EST AU082143 (E4368) corresponds to a region of the predicted gene. hypothetical protein" /codon start=1 /protein id="BAA90790.1" /db xref="G1:6983855" /translation="WAELPPNDDAIVMQDKEEEVEEKIVEEEKPSAPAAEVNNTEVVB FTIEWKNTPUNGTTEVNKSEEEKPIQS" join(1092. 1123,1482. 1740,1821. 2060) /note="hypothetical protein" /protein id="BAA90791.1" /protein id="BAA90791.1" /protein id="BAA90791.1" /db xref="G1:6983856" /translation="WDDQLDRISWARPWXKSTDRSKGESAIVGOFGGDGDAIHRR GRIEPRRRVAEIHQQVCALVASNPSSRRRCSLSTCRRRDSIDMSSFCTIGIFLIDGGI | TASFLEGSNRISRQ11"  complement (join (28593254,32863498,35043752, 39234483,45464662)) /note="hypothetical protein" /codon serar=1 /protein id="BAA90792.1" /db xref="G1:6983857" /translation="MGRSGRAKWAGRFKTAQARARGRGGERGPVDRAHHARSRGRGGT RCTRAVRGGRGGGPTRSITARGGTRAREDIDRGRLDPALAVLAPTWRLAGCHAGRE VDDAGRANGRRSTAASDGANHGDTGKSEHTGREDAGCGGTRSTRR QPAAGEEBEORGAPTRSITARGGTRAREDIDGGGGGRRRRREFTRARAATA QPAAGEEBEORGAPTRAREGAFRLRESDASVGGGTPRSTARELEGGGSRRR QPAGGEGGGAPTRATEBEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG                                                                                                                                                                                                                          | DAN"  DAN"  Complement (984812845)  /noce="3' LTR"  complement (join(1285716323,1838418477,1951320442))  /noce="Similar to 22 kDa kafirin cluster; Ty3-Gypsy type  (AF061282)  internal stop codon:15317-15319  probably inactive because stop codons are included in CDS"  /pseudo | /codon_start=1 complement(join(2071120932,2398724562)) complement(join(2071120932,2398724562)) /note="Similar to gypsy-type retrotransposon RIRE8B DNA, internal region (AB014741)" /codon_start=1 /protein_id="managengangangangangangangangangangangangangan                                                |
| COMMENT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | FEATURES SOURCE COS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | SOD                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | CDS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | LTR                                                                                                                                                                                                                                                                                 | CDS                                                                                                                                                                                                                                                                                                           |

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LPVVLTKDEGSRVVEEEAKESVHDDAGESSQVISSP"

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/codom fatarial
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SKERNRYVSTSTONVSTVIVRERHLAGGRAPPIVGMDFSRRYRGLYFGEBPDQRPML
VGSSICSAQFTMLRVLDLEMANPSYTOKDINKIGLLAHLRYLJATHFRRRSTIYALPS
IGKLQNLQVLDIRESEISTLPTDISKLLMLRILRSKGPWYFYFYFDPDEPIKCLKHT
LITMEPLALTPLUGSAARNYTIAELHRAYSSHWSETPGVRVPTGISKLEGLOULSVVDLK
LITKSRAIEELGELAULGKLAYSTKGADKRKTLCGAIEKLSSLGSLCVYSTYFTT
TLEMLGPCNPSPPPLAKLELHGRIRVMPDSFRNLKQLRKIPIRLSSLGSLCVYGTYFITG
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KLVGFDTPKKELLDKINMDANDDHCRVLCVVCMGGLCKTTLVRKIFESKEDIINNFP
HRAWIVVSQSFSMIEMLKDMISQLLGHESLKRFEGKPIRAHDLGTHLRDGLKELRYFV
                                                                                                                                                                                                                                             VPDDLWNTDHWEWIREFALPSKNNKRSRVIVTTRLDGVANACTTBPFVYRLKLLETEC
AIDLLLRKMGESKEDMKNDNNLKSIVTQLVKKCGCLPLAIVTICAMFANKPSSKWEEM
CRQLPSELENNPSPGVEAIRRVVTLSYGHLPSHLKPCYLYLSIPPEDIEIKRRHLVNR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGGATGTTCGGAATCATTCTCGTAGCAACATCGACGAAGCAAAGCTTGTAGGCTTTGAC
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| VERSION<br>KEYWORDS<br>SOURCE<br>ORGANISM                                                                                                                                                                                                                                                  | REFERENCE<br>AUTHORS                                                       |                                                  | TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS                            |                                                                            |                                                               |                                                 |                                                                         |                                                                            |                                                                          |                                                                          | TITLE<br>JOURNAL<br>COMMENT                                             |                                                                          |                                                      |                                                                                                                   |                  |                         |       |
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6248 bp mRNA linear PLN 24-JUL-2003 Oryza sativa (japonica cultivar-group) cDNA clone:J023064A19, full AK070885

DEFINITION

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and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Inmanra, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Kishikawa-Hirozane, T., Kojima, Y., Konno, H., Konno, H., Konda, M., Koya, S., Kurihara, C., Matsuyama, T., Myazaki, A., Murata, M., Nakhi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakain, Sand, H., Sand, H., Sand, K., Shibata, K., Shihata, K., Shihata, K., Shihata, K., Sand, H., Sand, K., Sand, H., Sagabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.
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Best Local Similarity 58.0%;
Matches 1421; Conservative
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Yamamoto,M.
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and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K.,
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Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Satoki, D., Satoki, K., Shinagawa, A., Shiraki, T., Yoshino, M. and Hayashizaki, Y. Coshino, M. and Hayashizaki, Y. Collection, mapping, and annotation of over 28,000 cDNA clones from
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Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (E-mail:8Ktuchi@milas.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007, This clone is one of the 28K full-length cDNA clones from japonica
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    1996 AGAGCAATCAAAGAGCTGGGGCAGTTAAGCAAGCTGAGGAAATTAGGTGTGATGACAAAT 2055
                                                                                                                                                                                                                                 ACCGAGAGGAATGTCAGTTAT----CTCTGTGAAGCCCTTCAGAAGCTTTCTTCTCTC 2896
                                                                                                                                                                                                                                                                                                                                                    2116 CAATATCTCTATGTGAATGCTGCAGGAATCTCAGATGGTGGAACACTTGAGTGCCTAGAT 2175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2176 TCTATTTCCTCTCCTCCTCCCCTACTGAGGACACTCGTGTTGTATGGAAGTCTTGAAGAG 2235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTAAAGGAAGGTAAAACCATGCTGATACTTGGGGCATTGCCCAACCTCATGGTCCTTGAT 2355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----Trgcrrccccaccrcccrccrcacaccrccrcaaarrgaaaggcrcccrrcargaa 3007
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Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Bukaryota, Viridiplantes, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Ehrhartoideae, Oryzeae, Oryza.
                                                         2783 AAAGCAGTCCACGAGTTGGGGGGAACTTACTCAGCTGAAAAAATTAGGCGTGGCAGGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                    2897 TGTTCCCTTCGTGTGGAGGCCAAACCCTTCCGAGGCCTCCACATGCTTGAGCAGC----
                                                                                                                                                                            2056 GCCTCGACAAAGGAAAATGTAAGATACTTTGTGCAGCCATTGAGAAAGCTCTTCCCTC
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PLN 28-APR-2003 disease

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Wieds Vej 10, DK-8000 C, DENMARK
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BINQLLGFELRQCLKELEBRAVHVEDLASYLREKLEDMRYETVLDDLWTIDAWDWI
KSTAFPIRNNKDSR LITTRDVGLARKCTSDSLIYHLKHLQIEDATNLLLRKSRKTWE
DMKNDKROMAVVNKOVRKCGGLPFALIT"
                                                                                                                                                                                                                  Hordeum vulgare
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Lillopsida, Poales, Poaceae,
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/protein_id="CAD44593.1"
/db_xref="GI:28555850"
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                                                                                                                                                                                                                                                                                                Madsen, L.H., Collins, N.C., Rakwalska, M., Backes, G., Sandal, N., Krussell, L., Jensen, J., Waterman, E.H., Jahoor, A., Pryor, A.J., Langridge, P., Schulze-Lefert, P. and Stougaard, J. Barley disease talesce gene analogs of the NBS-LRR class: identification and mapping Mol. Genet. Genomics 269 (1), 150-161 (2003)
                                                                                                   DNA linear
gene for NBS-LRR
                                                                                                                                                 AJ506137
AJ506137.1 GI:28555849
NBS-LRR disease resistance protein homologue; rga
Hordeum vulgare
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. 564
/organism="Hordeum vulgare"
/mol_type="genomic DNA"
/cultivar="Regatta"
                                                                                                HVUSO6137 564 bp
Hordeum vulgare partial rga S-9202
resiblerance protein homologue.
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Submitted (22-AUG-2002) Madsen L.H.
Biology, Aarhus University, Gustav
Location/Qualifiers
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1. .564
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/gene="rga
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2002 AGCATGATTCAAC
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                                    Gaps
                                    10;
 Length 2015;
 13.5%; Score 405.4; DB 8; Length 64.1%; Pred. No. 4.4e-95; ive 0; Mismatches 361; Indels
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                                    662; Conservative
                 Similarity
 Query Match
Best Local S
Matches 662
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Gaps

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Length 564;

180

591 237 651

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TVHRERREGUEMENTELRAKVEDVSQRNMRYHGVSAAAPQSSSYTAAELLQSTAAIDDI
DBARRAAKQOGKVDLVULITWOGQGLRVIAVLETRGGPAGTVPVVTAAYQKLKGEFE
CHAWVELAHEFDANOPIGSLVQRKANSREGTGKTPGGTPSGVSVLNEMEAGDYNLLH
DFTGYTVTNKKYLVVLOLSTIBEMDAIKTYLEPNAHOGSRVLVCTQQABVASCCTCTDD
OGVIQEDGPROLDPESSLPPHIANDSYNSDFTKKKSETRSSMEGASTTSDSKTVPS
DGVIQEDGPROLDPESSLPPHIANDSNTVSVKELSRSTTQLIGRGKEKDDVIKLLSDCN
PIROVISVWGMGGIGKTTLVKSIYQSSELEKLGFERRAWVTVLRPFQLTELLSDCN
IVKDSPGKKVBSIPGGARTLVKSIYQSSELEKLGFERRAWVTVLRPFGLTELLSDCS
SELKPDIKEBAKIITKKCGRLPLAMPCGFESRARMISIELTGOALLEITKTVRMGDE
SELKPDIKEBAKIITKKCGRLPLAMPTVGGFLSARPRNIIECTTGWBGDE
SELKPDIKEBAKIITKKCGRLPLAMPTVGGFLSARPRNIIECTTGREGOBLE
LEMIKKILLASSYEGLTYHLKGCFLYMSIPPEDSDIRYRRLLERWTAEGYSRATRNRSN
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LCSA ADMPRLQSLLLRABGNAGLEGCLDNNGSPPKDLKSLOLYGNIVTPEWIYDLKY
ILOKLSLRYTNLKADTYMEVLGNLPMLAILRLODNACEEEELCFGPBRFTGLTSLELL
NWESLKSVKPERGATPKLKVILLHYCWQIHNGGFSGIETLSTLKEVSILGYNYDQTYT
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TSRSKDKVRHLVVSKSWSREKNDMQNIVDVSHIRSLTVFGEWKSFFLSKKMRMLRVLD
                                                                                                                       /db_xref="G1:7415941"
/translation="MEATAVSVGKSVLGGALSYAQTAIAEEGALKLGVQRDQSFIRDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PATIGRLQNLKYVHAGSLDDEDDQPIIKLLHQFRSIREEMGTRFAVSYIMLFITAWLR
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                                                                                                                                                                        LEMMOSFILLAADKEHDGHHHEVIRTWVKQVRDVAYDVEDCLODYAARLKKPPWWSLPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEDAEGLODPDLVPIGKLHHLKYLSLRGSFGVFNLPNSFGNLLNLETLDIRGTWVTKL
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                                              /note="NBS-LRR type resistance gene"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.7%; Score 202.2; DB 8;
llarity 46.5%; Pred. No. 1.7e-41;
Conservative 0; Mismatches 1118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EFKEQLQKQLDMNKNKPNLSIL"
                                                                                             /protein_/
/db_xref='
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Matches 1023;
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                                                                                                                                                                                                                                                                                                                                                   891
                                                                                                                                                                                                                                                                                                                                                                                                 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                               298 GATTGGATCAAATCTATTGCTTTTCCTATTAGAAACAATAAAGACAGCCGAATATTAATA 357
238 AAGCTAGAGGACATGAGATACTTTATTGTTCTTGATGACTTGTGGACCATAGATGCTTGG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hayasaka,H., Katayose,Y. and Sasaki,T. The Pib gene for rice blast resistance belongs to the nucleotide binding and leucine-rich repeat class of plant disease resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (28-APR-1998) Takuji Sasaki, National Institute of Agrobiological Resources, Nice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@abr.affrc.go.jp, Tel:0298-38-7441,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang, Z.X., Yamanouchi, U., Katayose, Y., Sasaki, T. and Yano, M. Expression of the Pib rice-blast resistance gene family is up-regulated by environmental conditions favouring infection and chemical signals that trigger secondary plant defences Plant Mol. Biol. 47 (5), 653-661 (2001)
                                                 AATTGGATAAATGAAATTGCATTTCCTAAGAACAATAAGAAGGGCAGTCAAATAGTAATA
                                                                                                                                                ACCACTTGGAATGTTGATCTTGCGGAGAAGTGTGCCACAGCCTCACTGGTGTACCACCTT
                                                                                                                                                                                                                                                   GATTTCTTGCAGATGAACGATGCCATAACATTGCTACTGAGAAAAACAAATAAAAATCAT
                                                                                                                                                                                                                                                                                                    GAAGACATGGAATCAAATAAAAATATGCAAAAGATGGTTGAACGAATTGTAAATAATGT
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/clonne="PCT2005"
/tissue_type="green leaf"
/clonne_lib="cDNA leaves inoculated with Pyricularia
griceaJapanese Race 003, PC90-18C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang, Z.X., Yano, M., Yamanouchi, U., Iwamoto, M., Monna, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa PibH8 mRNA, complete cds.
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/mol_type="mRNA"
/strain="Tohoku IL-9"
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The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team; Kikuchi,S., Satch,K., Nagate,T., Kawagashira,N., Doi,K., Kikuchi,S., Satch,K., Nagate,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Li,C., Ohtsuki,K., Shishiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group: Otomo,Y., Murakami,K., Ilda,Y., Sugano,S., Pujimura,T., Suzuki,Y., Tamoda,Y., Kurosaki,T., Kodama,T., Mazuno,K., Yokomizo,S., Niikura,J., Kusumegi,T., Oka,M., Rawanata,M., Yokomizo,S., Niikura,J., Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RikEN:, Kawai,J., Kondo,S., Konno,H., Miyazaki,A., Osatco,N., Ota,Y., Saito,R., Sastco,R., Shinagawa,A., Shiraki,T., Voshino,M. and Hayashizaki,Y., Shibata,K., Shinagawa,A., Shiraki,T., Voshino,M. and Hayashizaki,Y.
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Oryza sativa (japonica cultivar-group) cDNA clone:J013043101, full
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Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head claboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@mias.affrc.go.jp, Fax:81-29-838-7007, Fax:81-29-838-7007)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          335 AGGTAATCTGTGTTGTTGGGATGGTGGTTTAGGCAAGACAGCTCTTTCGAGGAAGATCT
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'organism="Oryza sativa (japonica cultivar-group)"
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ull-Length cDNA Project Team:,
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hira, N., Kawai, J., Kawamata, M.,
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iahi, A., Yazaki, J., Yokomizo, S. and jp/cDNA/
tt Team: Kikuchi,S., Satch,K.,
 Kishimotc,N., Yazaki,J.,
 Hotta,I., Kojima,K., Namiki,T.,
 Li,C., Ohtsuki,K., Shishiki,T. and mRNA linear PLN 24-JUL-2003 roup) cDNA clone:J033067K01, full on of over 28,000 cDNA clones from iroup) phyta; Embryophyta; Tracheophyta; .Lopsida; Poales; Poacese; kuchi, National Institute of int of Molecular Genetics, Head of 1-2 Kannondai, Tsukuba, Ibaraki -length cDNA clones from japonica Tanama. Sequencing & Analysis Group: Otomo,Y., Iida,Y., FAIS Genome Sequencing & Ishibiki,J., Kawamata,M., Kobayashi,M., nias.affrc.go.jp,

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Yoshimura, A.
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/mol_type="mRNA"
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iive 0; Mismatches 354; Indels 18;
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Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
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Direct Submission
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Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
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/mol_type="mRNA"
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Search completed: Pebruary 13, 2005, 07:09:12 Job time : 8474.77 secs

Aaz58293 Sorghum r
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Aaz4679 Blast dis
Aaz50262 Coding re
Aaz50653 Genomic D
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Aag03715 DNA encod
Aag03715 DNA encod
Aag03715 DNA encod

Scoring table:

Searched:

Database

Perfect score:

Sequence:

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Pi2; NBS6; plant protectant; gene therapy; rice; disease resistance;
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AASO3713
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ABL50542
AAZ37153
AAS37153
AAS03715
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ABL50547
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ABL50549
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                                              AAA11350
AAZ50262
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AAZ50653
AAZ50264
ABL50546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-SEP-2002; 2002US-0409216P.
18-MAR-2003; 2003US-0455713P.
05-SEP-2003; 2003US-00656394.
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P-PSDB; ADM72249.

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 Adm72248 O. minuta
Adi57171 Oryza min
Adi57126 Oryza min
Adm72240 O. minuta
Adm72240 O. minuta
Adi57175 Oryza min
Adi57173 Oryza min
Adm72250 O. minuta
Adi57173 Oryza min
Adm72250 O. minuta
Adi57173 Oryza min
Adm72250 O. minuta
Adi57180 Oryza min
Adm7234 O. minuta
Adm7234 O. minuta
Adm7234 O. minuta
Adm7234 O. minuta
Adm7234 O. minuta
Adm7231 Oryza min
Adm7234 O. minuta
Adm7234 O. minuta
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Adm7224 O. minuta
                                                                                                               February 12, 2005, 22:05:25; Search time 1007.47 Seconds (without alignments) 17609.842 Million cell updates/sec
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            GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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Match
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Score

Result No.

2401.4 2401.4 2401.4 23401.4 2347.6 2347.6 2347.6 2347.6 10103.4 10103.4 333.4 333.4 1099.1 1099.1 1099.1 1099.1 1099.1 1099.1

New rice Pi2-like disease resistance nucleic acid molecule that confers disease resistance in plants, useful for creating or enhancing disease resistance in plants.

Claim 1; SEQ ID NO 11; 120pp; English

| q <sub>0</sub>    | 901  |                                                                       |
|-------------------|------|-----------------------------------------------------------------------|
| ò                 | 961  | 10                                                                    |
| ф                 | 961  | AAATTCTATGAACACCTTCCTTCAGAACTAGAAATAAACCCAAGCCTGGAAGCTTTGAGG 1020     |
| ò                 | 21   | 080                                                                   |
| Ωp                | 21   | TAGGTTACAACCACCTACCATCCCATCTGAAACCATGCTTTTTGTAT 108                   |
| & 43              | 1081 | CTAAGTATCTTTCCTGAGGATTTTGAAATCAAAAGAATCGTCTAGTAGGTAG                  |
| 8                 | 1141 | TTTGTTAGACCAAAGGTTGGGATGACGACTAAGGATGTCGGAGAAAGTTAC 120               |
| qq                | 1141 |                                                                       |
| ò                 | 1201 | TITAATGAGCTAATCAACCGAAGTATGATTCAACGATCAAGAGTGGGCATAGCAGGAAAA 1260     |
| οg                | 1201 | TITAATGAGCTAATCAACCGAAGTATGATTCAACGATCAAGAGTGGGCATAGCAGGAAAA 1260     |
| ò                 |      | ñ                                                                     |
| <b>Q</b>          | 1261 | TTAAGACTTGTCGAATTCATGATATCATCCGTGATATCACAGTTTCAATCTCGAGA              |
| <u>ئ</u> ۾        | 1321 | GAAAATTTTGTATTGTTACCAATGGGAGATGGCTCTGATTTAGTTCAGGAAAACACTCGC 1380<br> |
| ò                 | 1381 | CATAGCATTCCATGGGAGTATGTCCTGCAAAACAGGATTGGATTGGAGCATTATTCGA            |
| Dp                | 1381 |                                                                       |
| ò                 | 1441 | CATTAGCTATTTTTGGTGACAGA                                               |
| Op                | 1441 | ITAGCTATTTTTGGTGACCCAAGAGTCTAGCACATGCAGTTTGTCCAGAT                    |
| ò                 | 1501 |                                                                       |
| Пр                | 1501 | <u> rgaggargitacgggreitggatetrgaggatgreatetraateaeteaaaaga</u>        |
| ò                 | 1561 | TTCGACCGTATTGCATTGTTGTGCCACTTGAAATACTTGAGTATTGGATATTCGTCATCC 1620     |
| Dp                | 1561 | rcacceraricariergecacirgaaracricaerariegararicercare                  |
| ò                 | 1621 | ATATATTICACTICCCAGATCCATIGGTAAACTACAGGGCCTACAAACTITGAACATGCCG 1680    |
| අු                | 1621 | - ריז                                                                 |
| ờ                 | 1691 | 74                                                                    |
| q                 | 1681 | aagtgagarcagtaaactcca                                                 |
| č                 | 1741 | CAACTITAGICTAAACCACCCAAIGAAGIGCAIA 180                                |
| QQ                | 1741 | rgacaactriagictaaaccacccaargaagigcaia 180                             |
| ờ                 | 1801 | AGTATTCACACCTTTAGTTAGTCGCGATGATCGTGCA 186                             |
| ОР                | 1801 | CTAACACAATATGCCTGCCTAAAGTATTCACACCTTTAGTTAG                           |
| ò                 | 1861 | ATACAAATTGCTGAATTGCACATGGCCACCAAAAGTTGCTGGTATAAATCATTCGGTGTG 1920     |
| Ор                | 1861 | <u>caaattgctgaattgcacatggccaccaaaagttgctggtataaatcattcggtgt</u>       |
| که م <sup>2</sup> | 1921 | AAGGTACCCAAAGGAATAGGTAAGTTGCGAGACTTACAGGTTCTAGAGTATGTAGATATC 1980<br> |
| ò                 |      | CAGTTAAGCAAGCTGAGGAAATTA 204                                          |
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CTTGGCCCCAGTTCTCTGGATCAACTCTTGCAAGAATTGCAAGGGAAGGTGGTGGTAA
 (first entry)
                                                                                                                                                 (WANG/) WANG G. (LIUG/) LIU G.
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The invention comprises the amino acid and coding sequences of nucleotide binding site (NBS) proteins from the Oryza minuta Pi9 locus (bacterial blight and rice blast resistance genes). The DNA sequences may be used as markers for resistance to infection with Magnaporthe grises in plant breeding programs. The present DNA sequence represents an NBS gene from the Oryza minuta Pi9 locus. 261 486 321 546 381 909 441 999 501 726 561 CTTGTTGGGTTTTCTGACTCCAAGAAAGGCTGCTTGAAATGATCGATACCAATGCTAAT TCGAGGAAGATCTTTGAAAGCGAAGAAGACATTAGGAAGAACTTCCCTTGCAATGCTTGG Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, Ni and NBS3, useful for producing plants resistant to Magnaporthe grisea 202 ATAGATTCCTATGCAGAAGACATTCGCAATCAATCAGCTCGAAATGTGGATGAAGCTGAG CTTGTTGGGTTTTCTGACTCCAAGAAAGGCTGCTTGAAATGATGGTACCAATGCTAAT GATGGTCCGGCCAAGGTAATCTGTGTTGTTGGGATGGGTGGTTTAGGCAAGACAGCTCTT GATGGTCCGGCCAAGGTAATCTGTGTTGTTTGGGATGGGTGGTTTAGGCAAGACAGCTCTT TCGAGGAAGATCTTTGAAAGCGAAGAGACATTAGGAAGAACTTCCCTTGCATTGCTTGG ATTACAGTGTCACAATCATTTCACAGGATTGAGCTACTTAAAGATATGATACGCCAACTT ATTACAGIGICACAATCATTICACAGGATTGAGCTACTTAAAGATATGATACGCCAACTT blast; Gaps Length 3096; ö nucleotide binding site; NBS; Pi9 gene; bacterial blight; rice plant breeding; transgenic plant; plant; gene; ds. C; 730 G; 800 T; 0 U; 0 Other; Oryza minuta Pi9 locus nucleotide binding site (NBS) gene 91; Indels DB 12; 80.1%; Score 2401.4; 96.4%; Pred. No. 0; iive 0; Mismatches Claim 3; SEQ ID NO 88; 136pp; English 25-JAN-2002; 2002US-0352106P. 01-FEB-2002; 2002US-0353304P. Sequence 3096 BP; 960 A; 606 27-JAN-2003; 2003US-00352179. Best Local Similarity 96.4 Matches 2456; Conservative WPI; 2004-121064/12. P-PSDB; ADI57172. US2004006788-A1

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ADI57171 standard; DNA; 3096

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                                                                                                                 nucleotide binding site; NBS; Pi9; bacterial blight; rice blast; plant breeding; transgenic plant; plant; ds.
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Pred. No. 0;
0; Mismatches
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                                                                                          genomic DNA
                BP.
                ADI57166 standard; DNA; 76272
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01-FEB-2002; 2002US-0353304P.
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Local Similarity 96.4%;
hes 2456; Conservative (
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                                                                (first entry)
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(LIUG/) LIU G.
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The invention relates to novel broad-spectrum resistance gene Pi2 and the NBS(1-6) genes present in the Pi2 gene cluster region. The rice Pi2-like disease resistance nucleic acid molecules are useful for enhancing disease resistance in plants. The present sequence represents a Pi2 region contiguous sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         497 AACTICITGGCCCCAGIICICIGGAICAACICITGCAAGAAIIGCAAGGAAGGIGGIGGIGG 556
                                                                                                                                                                                                                                                                                                                                                                                                                             New rice Pi2-like disease resistance nucleic acid molecule that confers disease resistance in plants, useful for creating or enhancing disease resistance in plants.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pi2; NBS1; plant protectant; gene therapy; rice; disease resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 99090 BP; 28990 A; 20403 C; 21246 G; 28450 T; 0 U; 1 Other;
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96.2%; Pred. No. 0;
cive 0; Mismatches
 42033 GCAGATCCTGTTCCTGATGCCGAAGGA 42059
                                                                                                                                        O. minuta Pi2 region contiguous sequence.
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                                                              DNA; 99090
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18-MAR-2003; 2003US-0455713P.
05-SEP-2003; 2003US-00656394.
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                                                                                                               (first entry)
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Best Local Similarity 96.2
Matches 2454; Conservative
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     | Oy 2177 CTATTICCTCTCCTCCTCCTACTGAGGACACTCGTGTTGTATGGAAGTCTTGAAGAGA 2  D) 19919 CTATTTCATCTCCTCCTCCTCTACTGAGGACACTCGTGTTGGATGAATTCTTGAGGAGA 7 | Oy 2237 IGCCTAACTGGATTGAGCAGCTCACTCAACTGAAGAAGATCTACTTATTGAGGAGCAAAC 2 | Qy 2297 TAAAGGAAAGTAAAACCTGATACTTGGGGCATTGCCCAACCTCATGGTCTTGATC 2 | Qy 2357 TTTATCGGAAAGCTTACCTTGGGGAGAAGCTAGTATTCAAAACAGGGCATTCCCAAATC 2 | OY 2417 TTAGAACACTTTCGATTTACGATTTGGATCAGCTAAGAGAGATTAGATTTGAGGACGGCA 2 | OY 2477 GCTCGCCCCACTTGGAAAGATAGAAATCAGATTCTGCAGGTTGGAATCAGGGATTATTG 2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                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           | Qy       2657       GGGAGGACCGAAGTGATCACGACCTTGCTTGTGACGCCGAAGGATCCTCCTGTTGAAGTGG       2         Db       80399       ACAGTGACCGAAGGTATCACGACCTGGGGGCTGAAGGCCGAAGGATCTTCTATAGAAGTGC       8 |
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GIGACAGACCCAAGAGICTAGCACATGCAGTTIGICCAATTGAGGATGTTACGGGGTTCTTAGGATGTTACGGGGTTCTTAGGATGTTTGAGATGTTAGGATGTTACGGGGTTTCGAGAAAGATTTCGACGTATTGCATTAGGATGTTTTTAGGATGTTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTTAGGATGTAGGATGTAGGATGTAGGATGTAGGATGTAGGATGTAGGATGTAGGATGTAGGATGTAGGATGTAGGATGTAGGATGTAGGATGTAGGATGTAGGATGTAGGATGTAGGATGTAGGATGTAGGATGTAGGATGAGATGTAGGATGTAGGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAGATGAGAGATGAGATGAGATGAGATGAGAGATGAGATGAGATGAGAGAAGA | 79255 TCTTGGATCTTGAAGATGTGACATTCTTAATCACTCAAAAAGATTTCGACCGTATTGCAT 79318<br>1577 TGTTGTGCCACTTGAAATACTTGAGTATTGGATATTCGTCATCCATATATTCACTTCCCA 1636<br>                                       |
| q &                                                                                                                                                                                                                                                                                                                                      | සු දු ස                                                                   | 3 8 8                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           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     | ) & A                                                                                                                                        | <b>강</b> 원                                                             | දු දු                                                             | · 상 원                                                                 | े हे ह                                                                 | 3 & 5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                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            CTCTTTCGAGGAAGATCTTTGAAAGCGAAGAAGACATTAGGAAGAAGAACTTCCCTTGCAATG
                                                                                                                                                           TGCAAGTACATCATCTTTCTGAGTACCTGATAGAAGAGGCTCAAGGAGAAAGAGGTACTTTG
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CTCTTTCGAGGAAGATCTTTGAAAGCGAAGAAGACATTAGGAAGAACTTCCCTTGCAATG
                                                             CTTGGATTACAGTGTCACAATCATTTCACAGGATTGAGCTACTTAAAAGATATGATACGCC
                                                                                                                                             TGCAAGTACATCATCTTTCTGAGTACCTGATAGAAGAGCTCAAGGAGAAGAGGTACTTTG
                                                                                                                                                                                                                                                                                                                                          TAACATTGCTACTGAGAAAAAACAAATAAAAATCATGAAGACATGGAATCAAATAAAAATA
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                                              CTTGGATTACAGTGTCACAATCATTTCACAGGATTGAGCTACTTAAAGATATGATACGCC
                                                                                                                                                                                                                                           CTAAGAACAATAAGAAGGGCAGTCAAATAGTAATAACCACTTGGAATGTTGATCTTGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel broad-spectrum resistance gene Pi2 and the NBS(1-6) genes present in the Pi2 gene cluster region. The rice Pi2-like disease resistance nucleic acid molecules are useful for enhancing disease resistance in plants. The present sequence represents a cDNA encoding a rice NBS4 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGAGCTTGTTGGGTTTTCTGACTCCAAGAAAGGCTGCTTGAAATGATCGATACCAATG 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New rice Pi2-like disease resistance nucleic acid molecule that confers disease resistance in plants, useful for creating or enhancing disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTAATGATGGTCCGGCCAAGGTAATCTGTGTTTGTGGGATGGGTGGTTTAGGCAAGACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTAATGATGGTCCGGCCAAGGTAATCTGTGTTGGGATGGGTGGTTTAGGCAAGACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                             Pi2; NBS4; plant protectant; gene therapy; rice; disease resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 12; Length 3099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3099 BP; 954 A; 613 C; 743 G; 789 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 79.9%; Score 2393.6; Best Local Similarity 96.1%; Pred. No. 0; Matches 2453; Conservative 0; Mismatches
                            AAACAGCAGATCCTGTTCCTGATGCCGAAGGA
            AAGCAACGGATCCCCTCCCAGAGCAGGAGGA
                                                                                                                                                                     O. minuta NBS4 polypeptide encoding cDNA
                                                                                                                                                                                                                                                     Location/Qualifiers
1. .3099
/*tag= a
/product= "NBS4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 7; 120pp; English.
                                                                                              ВР
                                                                                              standard; cDNA; 3099
                                                                                                                                                                                                                                                                                                                                                                                        09-SEP-2002; 2002US-0409216P.
18-MAR-2003; 2003US-0455713P.
05-SEP-2003; 2003US-00656394.
                                                                                                                                                                                                                                                                                                                                                                  08-SEP-2003; 2003WO-US027913
                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                        (OHIS ) UNIV OHIO STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   resistance in plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-257576/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; ADM72245.
                                                                                                                                                                                                                                                                                                                   WO2004022715-A2
                                                                                                                                                                                                                                  Oryza minuta
                                                                                                                                              03-JUN-2004
                                                                                                                                                                                                                                                                                                                                          L8-MAR-2004
           2717
                                                                                                                     ADM72244;
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                                                                                                                                                                                                          gene;
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Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2 and NBS3, useful for producing plants resistant to Magnaporthe grisea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention comprises the amino acid and coding sequences of nucleotic binding site (NBS) proteins from the Oryza minuta P19 locus (bacterial blight and rice blast resistance genes). The DNA sequences may be used a markers for resistance to infection with Magnaporthe grisea in plant breeding programs. The present DNA sequence represents an NBS gene from the Oryza minuta P19 locus.
                                                                                                          2657 GGGAGGACCGAAGTGATCACGACCTTGCTTGTGACGCCGAAGGATCCCCTGTTGAAGTGG
                                                                                                                                   2882 ACAGTGACCGAAGGTATCACGACCTGGGGGCTGAAGCCGAAGGATCTTCTATAGAAGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGAGCTTGTTGGGGTTTTCTGACTCCAAGAAAAGGTTGCTTGAAATGATGATGATACAATG
                                                             GCCTTGCTCAGCTGGAGGAGGAGAGTGAACGCACACCCAAATCGCCCCGTGCTGCTAATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGAGCTTGTTGGGTTTTCTGACTCCAAGAAAAGGCTGCTTGAAATGATCGATACCAATG
   GTATCATTCACCTTCCAAAGCTCAAGGAGATTCCAATTAGATACGGAAGTAAAGTGGCTG
                                          GGCTTGCTCAGCTGGAGAGAGAGTGCGCACACACCCAAATCACCCCGTGCTGCGAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                blast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 3276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleotide binding site; NBS; Pi9 gene; bacterial blight; rice plant breeding; transgenic plant; plant; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3276 BP; 1028 A; 631 C; 770 G; 847 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza minuta Pi9 locus nucleotide binding site (NBS) gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
79.3%; Score 2377.6; DB 12; Lengt
Best Local Similarity 95.7%; Pred. No. 0;
Matches 2443; Conservative 0; Mismatches 109; Indels
                                                                                                                                                                                     AAGCAACGGATCCCCTCCCAGAGCAGGGGA 2748
                                                                                                                                                                                                                       AAACAGCAGATCCTGTTCCTGATGCCGAAGGA 2973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; SEQ ID NO 92; 136pp; English.
                                                                                                                                                                                                                                                                                                                   BP.
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01-FEB-2002; 2002US-0353304P.
                                                                                                                                                                                                                                                                                                                   ADIS7175 standard; DNA; 3276
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                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (WANG/) WANG G. (LIUG/) LIU G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza minuta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-JAN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infection
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   2762
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disease resistance in plants, useful for creating or enhancing disease
resistance in plants.
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18-MAR-2003; 2003US-0455713P.
05-SEP-2003; 2003US-00656394.
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95.4%;
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| 2362<br>2587<br>2422<br>2647<br>2482<br>2707                              | 2542<br>2767<br>2602<br>2827                                           | Oy 2852 GACCGANGGGATCA Db 2887 GACCGAAGGGATCA OY 2722 ACGGATCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC | RESULT 8 ADI57173 ID ADI57173 standard; DNA; XX XX XX DT 22-APR-2004 (first ent | XX XX XX XX XX XX XX XX XX XX XX XX XX                                     |                                                                                                                                                                                                                                                                                                                                                                          | A (WANG/) WANG G. PA (LIUG/) LIU G. XX PI Wang G, Liu G; XX DR WPI; 2004-121064/12. DR P-PSDB; ADI57174.                                                                                                                                                                                                                                                        | PT ANCLEIC acids encoding PT and NBS3, useful for pr infection.  XX XX Claim 3; SEQ ID NO 90; XX CT the invention comprises CC binding site (NBS) prot CC binding acide blast r CC blight and rice blast r CC blight and rice blast r CC blight and rice blast CC markers for resistance CC breeding programs. The CC the Oryza minuta Pi9 lo |
|---------------------------------------------------------------------------|------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------|----------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1282   GATATCATCCGTGATATCACAGTTTCAATCTCGACACAGAAATTTTGTATTGTTTACCA   1341 | 1462 AGACCCAAGAGTCTAGCACATGCAGGTTTGTCCAGATGATTGAGGATGTTACGGGTCTTG 1521 | 1582 TGCCACTTGAAATACTTGAGTATTGGATATTCGTCATATATTCACTTCCCAGATCC                                 | 1702   CCAAGTGAGATCAGTAAACTCCAANGTCTGCATACTCTTGGTTGTAGAAAGTTTGTT   1761         | 1822   AAAGTATTCACACCTTTAGTTTAGTCGCGATGATCGCGAATACAAATTGCTGAATTGCAC   1881 | 1942 AAGTTGCGAGACTTACAGGTTCTACAGTATGTAGATATCAGGCGGACCAGTAGTACAGC 2001  2167 AAGTTGCGAGACTTACAGGTTCTACAGGTATGTAGATATCAGGCGGACCAGTAGTAGAGCA 2001  2107 AAGTTGCGAGAGCTTACAGGTTCTAGAGTATGTAGATATCAGGCGGACCAGTAGTAGAGCA 2226  2002 ATCAAAGAGCTGGGGGCAGTTAAGCAAGCTAGGAAATTAGGTGTGATGACAAATGGCTCG 2061  2227 ATCAAAGAGCTGGGGGCAGTTAAGCAAGTTGAGGAAATTAGGTGTGATGACAAAAGGCTCG 2286 | 2062 ACAAAGGAAAATGTAAGATACTTTGTGCAGCCATTGAGAAGCTCTCTTCCCTCCAATAT 2121 2287 ACAAAGGAAAAATGTAAGATACTTTATGCAGCCATTGAGAAGCTCTCTTCCCTCCAATCT 2346 2122 CTCTATGTGAATGCTGCAGGAATCTCAGATGGTGGAACACTTGAGTGCCTAGATTCTATT 2181 2147 CTCTATGTGAATGCTGCAGAATGTTCAGATGATGAACACTTGAGTGCCTAGATTCTATT 2181 2347 CTCTATATGAATGCTGCGTTATTATCAGATATGAAACACTTGAGTGCCTAGATTCTATT 2406 | 2182 TCCTCCTCCTCCTACTGAGGACACTCGTGTTGTATGGAAGTCTTGAAGAGTGCCT 2241                                                                                                                                                                                                                                                                             |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               j nucleotide binding site (NBS) proteins NBS1, NBS2 producing plants resistant to Magnaporthe grisea
                   AGATAGAAATCAGATTCTGCAGGTTGGAATCAGGGATTATTGGTATT
                                                                                                                                                                                                                            TTGGGGAGAAGCTAGTATTCAAAACAGGAGCATTCCCAAATCTTAGA
                                                                    ACGATITIGGATCAGCTAAGAGAGAGATTAGATTTGAGGACGGCAGCTCG
                                                                                                                                                                                                       GGCTCAAGGAGATTTCACTTGGATACGAAAGTAAAGTGGCTGGGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleotide binding site (NBS) gene #4.
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| ପ୍ର                                                         | ò a                                                                  | <del>ර</del> සි                                                  | & a                                                              | & g                                      | <b>д</b>                                                                | <b>상</b> 옵                                                          | ò 8                                              | & g                                       | & ଶ                                                            | λο qq                                                                    | ò 8                                         | ኤ <sub>զզ</sub>                                                                                                           | & €                                                                                         | S G                                                       | S d                                                                                                                                     | <i>ት</i> ብ                                                    | <b>장</b> 옵                                                                    | ₩<br>6                                  |
| Sequence 3220 BP; 990 A; 616 C; 747 G; 867 T; 0 U; 0 Other; | 1%; Score 1411; DB 12; 1<br>1%; Pred. No. 0;<br>0; Mismatches 620; 1 | 206 ATTCCTATGCAGAAGACATTCGCAATCAGCTCGAAATGTGGATGAAGCTGAGCTTG 265 | 266 TTGGGTTTTCTGACTCCAAGAAAGGCTGCTTGAAATGATGATGATGATGATG 325<br> |                                          | 386 GGAAGATCTTTGAAAGCGAAGAGACATTAGGAAGAACTTCCCTTGCAATGCTTGGATTA 445<br> | 446 CAGTGTCACAATCATTCACAGGATTGAGCTACTTAAAGATATGATACGCCAACTTCTTG 505 | 506 GCCCCAGTTCTCTGGATCAACTCTTGCAAGAATTGCAAGGAAGG | atcatctttctgagtacctgatagaagagctcaagagagag | 626 ATGATCTATGGATTTACATGGATTGGATAAATGGAATTGCATTTCCTAAGAACA 685 | 686 ATAAGAAGGGCAGTCAAATAGTAATAACCACTTGGAATGTTGATCTTGCGGAGAAGTGTG 745<br> | ACTIGATITCTIGCAGAIGAAGGAIGCCATAACAITGC      | TACTGAGAAAACAAATAAAAATCATGAAGAATGGAATCAATAAAAATGAGAAAGATGAAAAGATGAAAAGATGAAAAGATGAAAAGATGAAAAGATGAAAAAGATGAAAAAGATGAAAAAA |                                                                                             | CTGTGCTTGCAACTAAACAGGTGTCAGAATGGGAGAAATTCTATGAACACCTTCCTT | AACTIGAGAATCAAACCTIGAAACATTAAGAGAATGGTGACCTAAGTTACAACCAAGGTTACAACAATGAGAATGGTGACCTTAGAGTTACAACCAATGAGAATGAGAATGAGCAAACCAAACAATGAGAAAGAA | ACCTACCATCCCATCTGAAACCATGCTTTTTGTAATCTAAGTATCTTTCCTGAGGATTTTG | AAATCAAAGGAATCGTCTAGTAGGTAGATGGATAGCAGAAGGGTTTGTTAGACCAAAGG<br>               | TCCGAGAAAGTTACTTTAATGAGCTAATCAACGAAGTA  |
| ΧX                                                          |                                                                      | & <del>8</del>                                                   | è 8                                                              | \$ A                                     | <i>è</i> 8                                                              | 충 A                                                                 | & B                                              | & <del>8</del>                            | & 8                                                            | <i>ት</i> ଶ                                                               | දි දි                                       | 8 8                                                                                                                       | 8 8                                                                                         | 8 8                                                       | 8 8                                                                                                                                     | & A                                                           | 8 8                                                                           | 8                                       |

AAATTAAGACTTGTCGAATTCATGATA 1285 | | | | | | | | | | | | | | SATTTTAAGAGCTGTCGAGGCA 1507 AAAGATTTCGACCGTATTGCATTGTTGT 1582 1632 AGGAAATTTTGTATTGTTACCAATGG 1345 GCCACATAGCATTCCATGGGAGTATGT 1405 1627 ATTCGATCATTAGCTATTTTTGGTGACA 1462 BATCAATTGAGGATGTTACGGGTCTTGG 1522 ACTITGAACATGCCGAGCACATACATT 1692 ATCTCTGCATACTCTTCGTTGTAGTAGA 1752 CCAATGAAGTGCATAACTAACAATA 1812 CGCGATGATCGTGCAATACAAATTGCT 1872 2091 TCTAGAGTATCTAGATATCAGGCGGAC 1988 AAGCAAGCTGAGGAATTAGGTGTGT 2048 ACTITIGICAGCCATIGAGAAGCICIC 2108 PGAGGACACTCGTGTTGTATGGAAGTCT 2228 ACTITAAAGAACTIATCAACCGIAGCA 1447 --AACAACATATTAACTAACACTTA 2031 AATCTCAGATGGTGGAACACTTGAGTG 2168 TCACCTGAAGATCTACTTATTGAG 2288 GGATATTCGTCATCCATATATTCACTT Accregaregretaaaacaariger

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disease resistance nucleic acid molecules are useful for enhancing
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                                  disease resistance in plants. The present sequence represents a fragment from the Pi2 region, that matched to NBS4.
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                                                                                        Sequence 2422 BP; 718 A; 492 C; 561 G; 635 T; 0 U; 16 Other;
                                                                                                                           Length
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 94.1%;
Matches 1407; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to novel broad-spectrum resistance gene Pi2 and the NBS(1-6) genes present in the Pi2 gene cluster region. The rice Pi2-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rice Pi2-like disease resistance nucleic acid molecule that confers ease resistance in plants, useful for creating or enhancing disease
                                                                                                                                                                                                                                                                                                                                                                                                                               GAGCAAACTAAAAGAAGGTAAAACCATGTTGGTACTTGCGGCGTTGCCCAACCTCATGGT
                                                                                                                                                                                                         GGACGCCAGCTCGCCCCAGTTGGAAAAGATAGAAATCAGATTCTGCAGGTTGGAATCAGG
                                                                                                                                                                                                                                                                                              GGACGCCACCTCAATCTTGCAAAAGATAGAAAT----ATTCAGGGTTGCAATCAGG
                                                                                                                                                                                                                                                                                                                                   GATTATTGGTATTATCCACCTTCCAAGGCTCAAGGAGATTTCACTTGGATAGGAAAGTAA
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                                                                                                                                CCTTTATCTTCATTCCAATGCTTACCATGGGGAGAAGCTAGTATTCAAAATGGGAGCATT
                                                                                                                                                                                CCCAAATCTTAGAACACTTTCGATTTACGATTTGGATCAGCTAAGAGAGTTAGATTTGA
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                                    GAGCAAACTAAAGGAAGGTAAAACCATGCTGATACTTGGGGCATTGCCCAACCTCATGGT
                                                                                                           CCTTGATCTTTATCGGAAAGCTTACCTTGGGGAGAAGCTAGTATTCAAAACAGGAGCATT
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18-MAR-2003; 2003US-0455713P.
05-SEP-2003; 2003US-00656394.
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                                                   The invention comprises the amino acid and coding sequences of nucleotide binding site (NBS) proteins from the Oryza minuta Pi9 locus (bacterial blight and rice blast resistance genes). The DNA sequences may be used as markers for resistance to infection with Magnaporthe grises in plant breeding programs. The present DNA sequence represents an NBS gene from
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Best Local Similarity 70.6%;
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                                                                                                                     GATCTACTTATTGAGGAGCAAACTAAAAGGAAGGTAAAACCATGCTGATACTTGGGGCACT
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2350 CTCCGTGTGCATGCTGAGGGATTCTCAGATACTGGAACACTTGAGTGGCTCAATTCGATT
                                                                              2470 AACTGGTTTGGGAACCTTAAGCAGCTGGTGAAGATGTGCTTATCCAGATGTGTGCTACAA
                                                                                                             CGGAAAGCTTACCTTGGGGAGAAGCTAGTATTCAAAACAGGAGCATTCCCAAATCTTAGA
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                     TCCTCTCCTCCTCCCTACTGAGGACACTCGTGTTGTATGGAAGTCTTGAAGAGATGCCT
                                                            AACTGGATTGAGCAGCTCACTCACCTGAAGAAGATCTACTTATTGAGGAGCAAACTAAAG
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                                                                                    The invention relates to novel broad-spectrum resistance gene Pi2 and the NBS(1-6) genes present in the Pi2 gene cluster region. The rice Pi2-like disease resistance nucleic acid molecules are useful for enhancing disease resistance in plants: The present sequence represents a cDNA encoding a rice NBS1 polypeptide.
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                                                                                                                                                                        Length 2982;
                              molecule that or enhancing d
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                                                                                                                                                   0 Other;
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Best Local Similarity 70.5%; Pred. No. 0;
Matches 1749; Conservative 0; Mismatches 727; Indels
                                                                                                                                                   T; 0 U;
                        disease resistance in plants, useful for creating resistance in plants.
                                                                                                                                                   Sequence 2982 BP; 917 A; 560 C; 733 G; 772
                                                                    Disclosure; SEQ ID NO 1; 120pp; English
WPI; 2004-257576/24.
P-PSDB; ADM72239.
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plant breeding; transgenic plant; plant; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217 GAAGACATICGCAATCAATCAGCTCGAAATGTGGATGAAGCTGAGCTTGTTGGGTTTTCT
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Pred. No. 2.2e-256;
0; Mismatches 788; Indels 90;
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    minuta NBS3 polypeptide encoding cDNA.

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TTATAACTAAAATAGTAAAGAAGTGTGGGTATTTACCGCTGGCTATACTCACAATAGGAG
                                              GCGTGCTTTCCACCAAAGAGATAAGAGAGTGGGAAACTTTTTATAGTCAGATACCTTCAG
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                                                                                                                                                                                                       The invention relates to novel broad-spectrum resistance gene Pi2 and the NBS(1-6) genes present in the Pi2 gene cluster region. The rice Pi2-like disease resistance nucleic acid molecules are useful for enhancing disease resistance in plants. The present sequence represents a cDNA encoding a rice NBS3 polypeptide.
                                                                                                                       New rice Pi2-like disease resistance nucleic acid molecule that confere disease resistance in plants, useful for creating or enhancing disease resistance in plants.
                                                                                                                                                                                                                                                                                                                                                                        TIGGGTTTTCTGACTCCCAAGAAAAGGCTGCTTGAAATGATGGTACCAATGCTAATGATG
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                                                                                                                                                                                                                                                                                                                     Length 4147;
                                                                                                                                                                                                                                                                                                                                                763;
                                                                                                                                                                                                                                                                                         Sequence 4147 BP; 1201 A; 831 C; 1029 G; 1086 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                     DB 12;
                                                                                                                                                                                                                                                                                                                   29.9%; Score 896.6; DB 12;
larity 60.6%; Pred. No. 3.8e-249;
Conservative 0; Mismatches 629;
                                                                                                                                                                               Example 4; SEQ ID NO 5; 120pp; English.
05-SEP-2003; 2003US-00656394
                           STATE
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P-PSDB; ADM72243.
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| 2470 GACGGCAGCTCGCCCCAGTTGGAAAAGATAGAAATCAGATTCTCGCGGTT 3289 GACGGCAGCTCAATCTTGTTGGAAAAGATAGAAATATTCAGGGTT 2530 ATTATTGGTATTATCCACCTTCCAAGGCTCAAGGAGATTTCACTTGGATP 3345 ATTGTTGGTATCATTCACCTTCCAAGGCTCAAGGAGATTTCACTTGGATP 3405 GTGGCTGGCTGGTGGTGGTGGGGGAAGTGCGCACACCCCAAATCA 2500 GTGGCTGGCTTGGTCAGCTGGTGGAGAGTGCGCACACCCCAAATCA 2600 GTGGCTGGCTTGGTCAGCTGGTGGAGGGTGCCCACCCCCAAGTG 3405 GTGGCTGGCTTGGTCAGCTGGTGGAGGCTCCCTTGTGACCCCAAATCA 2610 GTGGCTGGCTGGTCGCTGGAGGGAGAGTGCCCACCCCAC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Oy 2949 TTGTTTCANTCTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANTTGTANT |
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The invention comprises the amino acid and coding sequences of nucleotide binding site (NBS) proteins from the Oryza minuta Pi9 locus (bacterial blight and rice blast resistance genes). The DNA sequences may be used as markers for resistance to infection with Magnaporthe grisea in plant breeding programs. The present Oryza minuta DNA sequence was used in the exemplification of the invention.
                                                NBS1, NBS2
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                                                (NBS) proteins N
to Magnaporthe
                                              encoding nucleotide binding site in for producing plants resistant
                                                                                                              Disclosure, SEQ ID NO 97; 136pp; English
                 2004-121064/12
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Gaps Length 2351; 21; Sequence 2351 BP; 703 A; 420 C; 559 G; 651 T; 0 U; 18 Other; Score 844.2; DB 12; Length Pred. No. 4.8e-234; 0; Mismatches 568; Indels Query Match 28.2%; Best Local Similarity 68.1%; Matches 1256; Conservative

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1033 1093 1153 1213 1273 1393 ATGGGAGTAT---GTCCTGCAAAACAGGATTGGATTGGAGCATTATTCGATCATTAGCTA 1450 1507 1627 ŝ, GAATTCATGATATCATCCGTGATATCACAGTTTCAATCTCGAGACAGGAAAATTTTGTAT 1333 TGTTACGGGTCTTGGATCTTGAAGATGTGACATTCTTAATCACTCAAAAAGATTTCGACC 1567 913 973 184 244 364 424 484 604 664 124 CTGAGGATTTTTGATATCCAAAGGAAGCGCCTAGTACATAGATGGATTGCAGAGGGGTTTA 304 AAATAGGGTTGCTCACTTGAAATATGTGAATATTGGAGGGCATTCAAGTATTTATG 784 64 ATATGCAAAAGATGGTTGAACGAATTGTAAATAAATGTGGTCGTCTACCATTAGCAATAC TTACAATAGGAGCTGTGCTTGCAACTAAACAGGTGTCAGAATTGGGAAAATTCTATGAAC ACCTTCCTTCAGAACTAGAAATAAACCCAAGCCTGGAAGCTTTGAGGAGAATGGTGACCC TTAGAGCTAGGGGTGGAGTGGGAATTGTGGATGTGCCACAAAAGTATTTTGATGAGTTGA TCAACCGAAGTATGATTCAACGATCAAGAGTGGGCCATAGCAGGAAAAATTAAGACTTGTC TCAACCGAAGTATGATTCAAGCATCTAGAGTGGATATAGAGGGAAATATTAAGAGCTGCC GAGTCCATGATATCATGCGTGATGTCATGATATCTAGGGGAGGAAAATTTTGTAT TGTTACCAATGGGAGATGGCTCTGATTTAGTTCAGGAAAACACTCGCCACATAGCATTCC 485 ACTIGATGGGTGATGATGGAACTAGTGTAGTGGAGGAAATATTCGCCATTTAGTGCACC TTTTTGG---TGACAGACCCAAGAGTCTAGCACATGCAGTTTGTCCAGATCAATTGAGGA GRATTGCATTGTGCCACTTGAAATACTTGAGTATTGGATATTCGTCATCATATATT TTAGACCAAAGGTTGGGATGACGACTAAGGATGTCGGAGAAAGTTACTTTAATGAGCTAA 1034 1334 854 1094 245 1154 1214 1274 1394 1451 1508 1568 725 5 914 65 974 125 185 305 365 425 545 605 665

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| 1628 | CACTTCCCAGATCCATTGGTAAACTACAGGGCCTACAAACTTTGAACATGCCGAGCCAT 1687<br>  |
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| 1688 | ACAITGCAGCACTACCAAGTGAGATCAGTAAACTCCAATGTCTGCATACTCTTCGTTGTA 1747<br> |
| 1748 | GTAGAAAGTTTGTTTCTGACAACTTTAGTCTAAACCACCCAATGAAGTGCATAACTAAC           |
| 1808 | CAATAIGCCIGCCTAAAGTAITCACACCTITAGITAGICGCGAIGAICGIGCAATACAAA 1867<br> |
| 1868 | TIGCTGAATTGCACGTGGCCACCAAAGTTGCTGGTATAAATCATTCGGTG 1918               |
|      | TGAAGGTACCCAAAGGAATAGGTAAGTTGCGAGACTTACAGGTTCTAGAGTATGTAGATA 1978<br> |
| 1979 | TCAGGCGGACCAGTAGTAGCAATCAAAGAGCTGGGGCAGTTAAGCAAGC                     |
| 2039 | TAGGIGIGAIGACAAATGGCTCGACAAAGGAAAATGTAAGAIACITITGIGCAGCCAIIG 2098<br> |
| 2099 | AGAAGCTCTCTTCCTCCATATCTCTATGTATGCTGCAGGAATCTCAGATGGTGGAA 2158         |
| 2159 | CACTTGAGTGCCTAGATTCTATTTCCTCCTCCTCCCCTACTGAGGACACTCGTGTTGT 2218       |
| 2219 | ATGGAAGTCTTGAAGAGGATGCCTAACTGGATTGAGCAGCTCACTCA                       |
| 2279 | acttattgaggagcaaactaaaggaggtaaaaccatgctgatacttggggcattgccca 2338<br>  |
| 2339 | ACCTCATGATCCTTGATCTTTATCGGAAAGCTTACCTTGGGGAGAAGCTAGTATTCAAA 2398      |
| 2399 | CAGGAGCATTCCCAAATCTTAGAACACTTTCGATTTACGATTTGGATCAGCTAAGAGA 2458       |
| 2459 | 459 TTAGATTTGAGGCGGCGGCGCCCCGGTTGGAAAGATAGAAATCAGATTCTGCAGGT 2518<br> |
| 2519 | TGGAATCAGGGATTATTGGTATTATCCACCTTCCAAGGCTCAAGGAGATTTCACTTGGAT 2578     |
| 2579 | ACGAAAGTAAAGTGGCTGGGCTTGCTCAGCTGGAGGGGAAGTGCGCACACACA                 |
| 2639 | ACCCGTGCTGCGAAAGAGGAGGACCGAAGTGATCACGACCTTG 2683<br>                  |

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                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention comprises the amino acid and coding sequences of nucleotide binding site (NBS) proteins from the Oryza minuta P19 locus (bacterial blight and rice blast resistance genes). The DNA sequences may be used as markers for resistance to infection with Magnaporthe grisea in plant breeding programs. The present Oryza minuta DNA sequence was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 GGTACCCAAAGGAATAGGTAAGTTGCGAGACTTGCAGGTTCTAGAGTATGTAGATATCAG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTCTCTTCCCTCCAATCTCTATGTGAAAGGCTGCGTTATTATCAGATATTGAAAACACT 390
                                                                                                                                                                                                                                                                                                                                                                        Nucleic acida encoding nucleotide binding site (NBS) proteins NBS1, NBS2 and NBS3, useful for producing plants resistant to Magnaporthe grisea
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                                                                                                          nucleotide binding site; NBS; Pi9; bacterial blight; rice blast; plant breeding; transgenic plant; plant; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2265 BP; 638 A; 471 C; 558 G; 598 T; 0 U; 0 Other;
                                                                                     Oryza minuta Pi9 locus-related DNA sequence #1
                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 96; 136pp; English.
             ADI57179 standard; DNA; 2265 BP.
                                                                                                                                                                                                                                               25-JAN-2002; 2002US-0352106P.
01-FEB-2002; 2002US-0353304P.
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(LIUG/) LIU G.
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391 TGAGTGCCTAGATTCTATTTCATCTCCTCCTCCCTACTGAGGACACTCGGGTTGAATGG
                                                                              451 AAGTCTTGAAGAGATGCCTAACTGGATTGAGGCGCGCTCACCTCACCTGAAGAAGATCTACTT
                                                                                                                                                                                         511 ATTGAGGAGCAAACTAAAGGAAGGTAAAACCATGCTGATACTTGGGGCATTGCCCCAACCT
                                                                                                                                                                                                                                                                  2343 CATGGTCCTTGATCTTTATCGGAAAGCTTACCTTGGGGAGAAGCTAGTATTCAAAACAGG
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

SE i (bases 1 to 3159)

Ma,L., Wango,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X., and Wang,J.

An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis

Lu Unpublished (2004)

Contact: Chen Chen

Department of Bioinformatic

Beijing Institute of Genomics

Chinese Academy of Sciences, Beijing 101300, China

Tel: 86-10-80488576
                                                                                                                                                                                                                                                                                                                          CL964074 11near GSS 21-SEP-2004 OSIFCC010263 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
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         AZ047631
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AG210016 Oryza sat
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18448.290 Million cell updates/sec
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          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                      nucleic search, using sw model
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| AGCTCGCCCCAGTTGGAAAAGATAGAAATCAGATTCTGCAGGTTGGAATCAGGGATTATT | 2656 AGGAGGACCGAAGTCACCACCTTGTTGTGACGCGAAGGATCCCTGTTGAAGTG 2715  3064 GAGGAGCCGACCTCACGACCTTGGAGAAGGATCCCCTGTTGAAGTG 2715  3064 GAGGAGCCCACCACGACCTCACGACAGGAGAAGGATCACTCAGTGTAGAAATG 3123  2716 GAAGCAACGGATCCCCTCCCACAGCAGGAGAG 2751 | CL964072 CL964072 LOCUS CL964072 LOCUS CL964072 LOCUS CL964072 LOCUS CL964072 CUltivar-group) genomic, genomic survey sequence. CL964072 CL964072 CL964072 VERSION CL964072.1 GI:52382856 KEYWORDS GSS. SOURCE Oryza sativa (indica cultivar-group) CNGANISM Oryza, viridiplantae, Streptophyta, Embryophyta, Tracheophyta; | REFERENCE  The spermacrophyra; main application by the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the st | Tel: 86-10-80488559 Fax: 86-10-80488676 Email: chenchen@genomics.org.cn Rice genomic sequence. Class: exon-trapped. FBATURES 1. 2925 /organism="Oryza sativa (indica cultivar-group)" /db_xref="texon39940" /clone_lib="Oryza sativa Express Library" /note="Oryza sativa exon trapped genomic sequences" /note="Oryza sativa exon trapped genomic sequences" | Query Match         43.0%;         Score 1290.2;         DB 9;         Length 2925;           Best Local Similarity 70.5%;         Pred. No. 0;         0;         Alsmatches 728;         Indels 6;         Gaps 2;           Matches 1753;         Conservative 0;         Mismatches 728;         Indels 6;         Gaps 2;           Qy         205 GATTCCTATGCAGAAGATCTCCAATCGATCAGCAACCATGACGAACTT 495           Qy         265 GATGGGTTTTCTGACTCCAAGAAAAGGCTGCTTGAAATGATCGATACCAATGATACTAATGAT 324           Db         496 GTGGGGTTTGCCAAGAAAAGATGATGATGATAAGATGATCAATACTAATGAC 555           Qy         325 GGTCCGGCCAAGGTAAATGTGGTTGAAAGATAAGATAAG |

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Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Burartoideae; Oryzeae; Oryza.
Enrhartoideae; Oryzae; Liliopsida; Poales; Poaceae;
Brhartoideae; Oryzae; Liliu,X., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J.
An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
Unpublished (2004)
Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80488656
                                                           2832
                                                                                                     2661
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/mol_type="genomic DNA"
/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone lib="Oryza sativa Express |
/note="Oryza sativa exon trapped:
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63.7%; Pred. No. 1.6e-253;
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CCCAAGAGTCTAGCACATGCAGTTTGTCCAGATCAATTGAGGATGTTACGGGTCTTGGAT 1524
                                                                                                                                                                CTGGAAGATGCAAAATTCAAAATCAAAATGATATCAGGAATATAGGGTTGTTGCGC 1812
                                                                                                                                                                                                              CACTTGAAATACTTGAGTATTGGATATTCGTCATCCATATATTCACTTCCCAGATCCATT 1644
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AG208890 698 bp DNA linear GSS 09-AUG-2003 Oryza sativa (japonica cultivar-group) DNA, clone:NE4506 0 401_1A, 3' flanking sequence of Tos17 insertion in rice strain NE4506,
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                                                                                                                              301 GCCCAACCTCATGGTCCTTTATCTTTATCGGAATGCTTACCTTGGGGGAGAAGCTAGTATT 360
                                                                                                                                                                                                                                                                                                                                                                                361 CAAAACGGGAGCATTCCCAAATCTTAGAACACTTTGTATTTACGAATTGGATCAGCTAAG 420
                                         121 TGGAACACTTGAGTGCCTAGATTCTATTTCATCTCCTCCTCCCCTACTAAGGACACTCAG 180
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                              GATCTACTTATTGAGGAGCAAACTAAAGGAAGGTAAAACCATGCTGATACTTGGGGCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (16-ARR-2002) Akio Miyao, National Institute of Agrobiological Sciences, Molecular Genetics; 2-1-2, Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:miyao@affrc.go.jp, URL:http://tos.nias.affrc.go.jp/, Tel:81-298-38-7020, Pax:81-298-38-7020)
                                                                                  2334 GCCCAACCTCATGGTCCTTGATCTTTATCGGAAAGCTTACCTTGGGGAGAAGCTAGTATT
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Target Site Specificity of the Tos17 Retrotransposon Shows a Preference for Insertion within Genes and against Insertion is Retrotransposon-Rich Regions of the Genome Plant Cell 15 (8), 1771-1780 (2003)
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Miyao,A., Murata,K. and Hirochika,H.
Direct Submission
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                                           GCATTGCGGCTGCTTCAAGACCGAAGCAAATCGACTTGGGGCTCCCTGTAGTCCTGACG 2934
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                                                                                                                                AAAGACGAAGGCTCCAATGTTGAAGAGGAAGCAAAGGAATCCGTCCATGACGATGCCGGG 2994
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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/note="Similar to Similar to gene for Pib (AB013448)
(Oryza astiva (japonica cultivar-group)] (BAA90798.1)."
  -CTTGT
                                                                                     GACGCCGAAGGATCCCCTGTTGAAGTGGAAGCAACGGATCCCCTCCCCAGAGCAGGAGGGA
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/clone_lib= PCR product directly amplified from rice genomic_DNA"
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Target Site Specificity of the Tosl7 Retrotransposon Shows a Preference for Insertion within Genes and against Insertion il Retrotransposon-Rich Regions of the Genome
Plant Cell 15 (8), 1771-1780 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/strain="NB9007"
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GTGCTGCGAAAGAGGAGGACCGAAGTGATCACGACCTTG
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88.8%; Pred. No. 1.5e-134;
cive 0; Mismatches 70;
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/ao, A., Tanaka, K. and Hirochika, H.
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/db_xref="taxon:39947"
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AG210016.1 GI:32357206
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Direct Submission
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Best Local Similarity 88.8
Matches 588; Conservative
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/tissue_type="young leaves"
/dev_stage="2 week old seedlings"
/dev_stage="2 week old seedlings"
/lab_hogt="DH10B T1 phage resistant"
/clone_lib="OR_CBa"
/hocte="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII;
drk treated 36 hrs before harvest"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2138 CAGGAATCTCAGATGGTGGAACACTTGAGTGCCTAGATTCTATTTCCTCTCCTCCTCCCC 2197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2018 AGTTAAGCAAGCTGAGGAAATTAGGTGTGATGACAAATGGCTCGACAAAGGAAAATGTA 2077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2198 TACTGAGGACACTCGTGTTGTATGGAAGTCTTGAAGAGATGCCTAACTGGATTGAGCAGC 2257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2318 TGATACTIGGGGCATIGCCCAACCICAIGGICCTIGATCTTIAICGGAAAGCTIACCTIG 2377
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Enhartoldea; Oryzae; Oryza.

1 (bases 1 to 703)
Kim, H., Yu, Y., Wissotski, M., Yost, D., Stum, D., Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              578 AGCTAATTCAGTTAAGAAATTAAGCGTGACAACAAAAAGGCGCCACAAATAAGAAGTATC 519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         278 AGATACTTGGGGGACTGCCCAACCTTATGGTTCTTCGTCTTTATCGCAACGCATATGCTG 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   338 TTAAGCAGCTGGTGAAGATGTGCTTATCCAGATGTGGGCTAAAAGATGGTAAAACTATGG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGATATTTTGTGCAGGGATTGAGAAGCTCTCTTCTCTGCAATCTCTCGGGGGATGCTG
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                                                                                                                                                    OWAP project
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Fax: 520 621 1259
Email: http://genome.arizona.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Oryza rufipogon"
/mol_type="genomic DNA"
/db_xref="taxon:4529"
/clone="OR_CBa0055J06"
                                                                                                                                                                                                                                                                                                                                                                    PORNWRD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0055 row: J column: 06
Seg primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACCATGCTGATACTTGGGGGCATTGCCCAACCTCATGGTCCTTGATCTTTATCGGAAAGC 2369
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                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                               /note="The 3' end of retrotransposon Tos17 was found immediately upstream of this sequence."
                                          /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/strain="NE4506"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGATCACGACCTTGCTTGTGACGCCGAAGGATCCCCTGTTGAAGTGGAAG 2719
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                                                                                                                                                                                                                                                                                                         16.7%; Score 501.8; DB 9; Length 698; 85.7%; Pred. No. 7e-129; tive 0; Mismatches 93; Indels 0
                                                                                                         /cultivar="Nipponbare"
/db.xref="taxon.39947"
/clone="NE4506_0_401_1A"
/clone lib="PCR product directly amplified
genomic DNA"
  Location/Qualifiers
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/clone_lib="R21"
/note="Grgan: Shoot-root transition zone from young plants
(large insert library); Vector: pSport1; Site 1: Sal1;
Site 2: Not1; An unidirectional cDNA library generated
from [Shoot-root transition zone from young plants (large insert library)]. CDNA was prepared from poly4+ mRNA
using SuperScript Plasmid System Kit (Invitrogen). The
double-scrand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://sucest.lad.ic.unicamp.br/public"
                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharum officinarum
Bukaryota, Viridiplantee, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum, Saccharum officinarum
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                                                                                                                                                                                                                                                                                         CA147958 709 bp mRNA linear EST 24-SEP-2003 SCEZRZ1015C04.g RZ1 Saccharum officinarum cDNA clone SCEZRZ1015C04 CA147958
ACGAGAAAATGACATTCAGAAGGGGAACATTCCCAAATCTCAGGTGTCTTGATATTACT 159
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                                                                                                                                         Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br
Plate: 01s row: C column: 04
Seg primer: T7 Promoter Primer.
Location/Qualifiers
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                                                     ATTIGGATCAGCTAAGAGAGTTAGATTIGAGGACGCCAGCTCGCCCCAGTTGGAAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
                                                                                                                                                                                           TCAAGGAGATTTCACTTGGATACGAAAGTAAAGTGGC 2594
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The libraries that made SUCBST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
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/db_xref="taxon:4547"
/clone="SCEZRZ1015C04"
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatrophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (baess 1 to 663)
Wing,R.A. and Dean,R.A.
MAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
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2018 AGTTAAGCAAGCTGAGGAAATTAGGTGTGATGACAAATGGCTCGACAAAGGAAAATGTA
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Faxi: 864 656 4293
Smail: rwing@clemson.edu
Seq primer: GGAAACAGCTATGACCATG
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OP Ba0025003.r OP Ba Oryza punctata genomic clone OP Ba0025003 3', genomic survey sequence.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopaida; Poalea; Poaceae;

Brhartoideae; Oryzae; Oryza.

(bases 1 to 875)

SanMiguel, P., Westeramn, R., Kim, H., Yu, Y., Wissotski, M., Yost, D.,

Stum, D., Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C.,

Hatfield, J., Soderlund, C., Wing, R. and Jackson, S.A.

Omap Project - Purdue University

Unpublished (2004)

Jackson Laboratory
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915 W. State St., West Lafayette, IN 47907, USA
Tel: 7654963621
Fax: 7654967255
                                                                                                                                                          1367 AGGAAAACACTCGCCACATAGCATTCCATGGGAGTATGTCCTGC
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BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 161000 Std Brror: 0.00
Plate: 0025 row: 0 column: 03
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
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/organism="Oryza punctata"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTTAAACCCTTGAAATTAAGCTATGCAAAAGAGTTGCTTCTAAGGAAAGCCAATTAAAC 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   828 TCATGAAGACATGGAATCAAATAAAATATGCAAAAGATGGTTGAACGAATTGTAAATAA 887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACAGAAGATATAGGAAGGGATTAAAAGATGAGTGACATTATTACTAANATAGTAAAGAA 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             888 ATGTGGTCGTCTACCATTAGCAATACTTACAATAGGAGCTGTGCTTGCAACTAAACAGGT 947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230 TTGGGAAAAGTTACTTTAAAGAACTCATCAACCGTAGCATGATTCAGCCATCAAGAGCGG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    470 AAAAGAGTGGGAAACCTTTTATAGTCAGATACCTTCAGAGCTTGAAAGCAACCT
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                                                                                                                             (japonica cultivar-group) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 11.8*; Score 354.2; DB 8; Length 663; Best Local Similarity 72.8*; Pred. No. 1.9e-87; Matches 469; Conservative 0; Mismatches 174; Indels 1
                                                                                                                   /organism="Oryza sativa
/mol type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
                                                                                                                                                                                                                                                /clone="nbxb0093A15r"
                            High quality sequence stop: 2
Location/Qualifiers
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/mol type="garging by a mol type="garging by a mol type="taxon:4529"

/db_xref="taxon:4529"

/db_xref="taxon:4529"

/tissue type="young leaves"

/dev_stage="2 week old seedlings"

/dav_stage="2 week old seedlings"

/dav_stage="1 bhoung 11 phage resistant"

/clone lib="0R-CRa"

/note="Vector: pAGIBAC1; Site 1: HindIII; Site_2: HindIII;

drk treated 36 hrs before harvest"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         284 ACTGTGTCTCAGTCATTTGACAGGAAAGAAATTCTGAAACAAATGATGAGGCAACTTCTG 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTACTGAGAAAAACAAATAAAAATCATGAAGACATGGAAATCAAATAAAAATATGCAAAAG 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTACTAGCAAAGACAAACATAAGACTTGAAGACATGGAAAATGATGAGGACTTGGGCAGC 703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.4%; Score 342.8; DB 9; Length 737; llarity 69.6%; Pred. No. 3.1e-84; Conservative 0; Mismatches 207; Indels 3
                                                                                                                                       g
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
PCR PRimers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TCA TAA GGC ACC
Plate: 0089 row: H column: 17
Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.
                                                                                                                                                                                                        1. ./s/
/organism="Oryza rufipogon"
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                                                                                                                                                                              Location/Qualifiers
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hes 480;
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OR_CBa0089H17.f OR_CBa Oryza rufipogon genomic clone OR_CBa0089H17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1042 AACCACCTACCATCCCATCTGAAACCATGCTTTTTGTATCTAAGTATCTTTCCTGAGGAT 1101
                                                                                                                                                                                                                                                                                                                                        742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza rufipogon
Oryza rufipogon
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
I (bases I to 737)
Kim, H., Yu, Y., Wissotski, M., Yost, D., Stum, D., Rao, K., Luo, M.,
Jetty, R., Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and
                                                TTGATGACATGTGGAACACACATGACTGGGAATGGATTAAGGAATTTGCCTTTGCCTAGTA 417
                                                                                                                                                                                                                                                                                                                                                                                                                   802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      837
                          TTACAGTGTCACAATCATTTCACAGGATTGAGCTACTTAAAGATATGATACGCCAACTTC 502
                                                                                                                                                                                TAGATGATCTATGGATTTTACATGATTGGAATTGGATAAATGAAATTGCATTTCCTAAGA 682
                                                                                                                                                                                                                                                                                                                                                                             CAAACAACAAAAGGAGTCGGGTAATAGTAACAACTAGATTAGATGGTGTAGCTAATGCAT 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCACTACTGAACCATATGTCTACCGCCTTAAACTCCTAGAGATTGAGTGTGCCATAGATT 537
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Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
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CL197270 603 bp DNA linear GSS 06-JAN-2004 104 424 10943635 114 32333 078 Sorghum methylation-filtered library (LibiD: 104) Sorghum bicolor genomic clone 10943635, genomic survey
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                                                                                                                                                                               463
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Eukaryota, Viidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 603)
Budiman, M.A. Flick, E., Jones, J., Nunberg, A., Citek, R.W.,
Budiman, M.A., Flick, E., Jones, J., Nunberg, A., Citek, R.W.,
Robbins, D., Rohlfing, T., Bradford, K., Fries, J., McMenamy, J.,
Trani, L., Isak, A., Zimmerman, C., Lakey, N. and Bedell, J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Sorghum methylation-filtered library (LibID:
                                                                                                                                                            CATCATCTTTCTGAGAGTACCTGATAGAAGAGCTCAAGGAGAAGAGGTACTTTGTTGTTCTA
                                                                                                                                                                                                                                              GATGATCTATGGATTTTACATGATTGGAATTGGATAAATGAAATTGCATTTCCTAAGAAC
                                                                                                                                                                                                                                                                                                                                                                     AATAAGAAGGCAGTCAAATAGTAATAACCACTTGGAATGTTGATCTTGCGGAGAGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                          524 AACAACAGAGGTAGTCGCATAATAACAACACGAGATGCTGGCTTAGCTGGAAGGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         745 GCCACAGCCTCACTGGTGTACCACCTTGATTTCTTGCAGATGAACGATGCCATAACATTG
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Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbdell@cvingenomics.com
Plate: 424 row: c column: 19
Seq primer: M13/pUC Forward
Class: shorgun
High quality sequence stop: 603.
Location/Qualifiers
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/mol_type="genomic DNA"
/cultivar="ATx623"
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/clone="10943635"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sorghum bicolor (sorghum)
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                                                                                                                740 bp DNA linear GSS 16-AUG-2004
OR CBa0033P17.f OR CBa Oryza rufipogon genomic clone OR_CBa0093P17
5', genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (Bases 1 to 740)
Kim, H., Yu, Y., Wissotski, M., Yost, D., Stum, D., Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTTGGGTTTTCTGACTCCAAGAAAGGCTGCTTGAAATGATCGATACCAATGCTAATGAT 324
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larity 69.4%; Pred. No. 3.5e-84;
Conservative 0; Mismatches 209; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
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   704 ATAGTTACAAATTGGTAAAAGGGTGTGGT 733
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Plate: 0093 row: P column: 17
Seg primer: TAA TAC GAC TCA CTA TAG
Class: BAC ends.
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PCR PRimers
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Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
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Oryza rufipogon
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                                                                                          RESULT 11
CL861885
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AUTHORS
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CTACTAGCAAAGACAAACATAAGACTTTGAGACATGGAAAATGATGAGGACTTGGGCAGC 703
                                                                               Email: http://genome.arizona.edu
PCR PRimers
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Oryza rufipogon
Gukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 709)
Kim.H., Yu.Y., Wissotski,M., Yost,D., Stum,D., Rao,K., Luo,M.,
Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and
Wing,R.
                                                                                                                                                                                                                                                                                                                                                                                                       995 TAAACCCAAGCCTGGAAGCTTTGAGGAGAATGGTGACCCTAGGTTACAACCACCTACCAT 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCATCTGAAACCATGCTTTTTGTATCTAAGTATCTTTCCTGAGGATTTTGAAATCAAAA 1114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGAATCGTCTAGTAGGTAGATGGATAGCAGAAGGGTTTGTTAGACCAAAGGTTGGGATGA 1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGACTAAGGATGTCGGAGAAGTTACTTTAATGAGCTAATCAACCGAAGTATGATTCAAC 1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1235 GATCAAGAGTGGGCATAGCAGGAAAATTAAGACTTGTCGAATTCATGATATCATCGTG 1294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1295 ATATCACAGTTTCAATCTCGAGACAGGAAAATTTTGTATTGTTACCAATGGGAGATGGCT 1354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 GGAGGCGCCTGGTAGGTGGATGGATAGCAGAAGGGTTTGTTAAAAGCCAGGGATGGGGTGA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 ACATTGAGGAAGTTGGAATAGTTACTTCAATGAGCTAATCAACCCAAGTATGATTCAAC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              541 ATATCATAGTTTCTAGAGAGAAAAATTTGTGCTCTCGCCTAAGGATAATGTCA 600
                                                                                                                                   755 CACTGGTGTACCACCTTGATTTCTTGCAGATGAACGATGCCATAACATTGCTACTGAGAA 814
                                                                                                                                                                                                                          181 CGACTAAAAAGATAGGAGAGGGGAAAGTTTTTTGAAGAACTCCCTTCAGAACTTGAGA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                      241 GCAATCTAAGCCTTGAAGCAATGAGGAGGATGGTTACCCTGAGTTATGACCACTTGCCAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 CTCATCTTAAGCCATGTTTTCTGTACCTAAGCATCTTCCCTGAGGATTTTGAAATTCAAA 360
                                                                                                                                                                                                 815 AAACAAATAAAAATCATGAAGACATGGAATCAAATAAAAATATGCAAAAGATGGTTGAAC 874
                                                                                                                                                                                                                                                                   GAATTGTAAATAAATGTGGTCGTCTACCATTAGCAATACTTACAATAGGAGCTGTGG 934
                                                                                                                                                                                                                                                                                                                                     CGCTTATTTACCACCTTGAACCCCTTCAAATGGATGATGCTGTACATTTGCTGCTAAGGA 60
                                                                                                  Gaps
and electroporated into E. coli cells. This is methylation-filtered library."
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                                                                   Length 603;
                                                              Score 341.2; DB 9; Length
Pred. No. 8.1e-84;
0; Mismatches 163; Indels
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                                                                11.4%;
72.9%;
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Unpublished (2004)
Contact: Rod A. Wing
                                                                                                  Matches 439; Conservative
                                                                                 Best Local Similarity
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                                                                 Query Match
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KEYWORDS
SOURCE
ORGANISM
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JOURNAL
COMMENT
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CL801486
LOCUS
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ACCESSION

REFERENCE AUTHORS

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/mol Lype="genomic DNA"
/db xref="taxon:4529"
/db xref="taxon:4529"
/clone="toxon:4529"
/tissue type="young leaves"
/dev_stage="2 week old seedlings"
/lab host="DH10B TI phage resistant"
/clone lib="OR_CBa"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII;
drk treated 36 hrs before harvest"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               284 ACTGTGTCTCAGTCATTGACAGGAAAGAATTCTGAAACAAATGATCAGGCAACTTCTG 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATCATCTTTCTGAGTACCTGATAGAAGAGCTCAAGGAGAAGAGGAGTACTTTGTTGTTCTA 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 625 GATGATCTATGGATTTTACATGGAATTGGATAAATGAAATTGCATTTCCTAAGAAC 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 Gradacriraccaagacraaagargastracriaaacraaragargraaraka 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          227 AGGAAGGCATATGAAAACAAGGAACACAT---GAAGAACTTCTCGTGTTGTGCTTGGATC 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   505 GGCCCCAGTICTCTGGATCAACTCTTGCAAGAATTGCAAGGGAAGGTGGTGCAAGTA 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTACTGAGAAAAACAAATAAAAATCATGAAGACATGGAATCAAATAAAAATATGCAAAAG 864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           datticitacctagaagatgctcgcaatcgatagcaacactgacgggtagaactt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGAAGATCTTTGAAAGCGAAGAAGACATTAGGAAGAACTTCCCTTGCAATGCTTGGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  445 ACAGTGTCACAATCATTTCACAGGATTGAGCTACTTAAAGATATGATACGCCAACTTCTT
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Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 629 5595
Fax: 520 621 1259
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                                                                                                                                                                                                   FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0013 row: H column: 04
Seg primer: TAA TAC GAC TCA TAG
Class: BAC ends.
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1. 709
/organism="Oryza rufipogon"
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1402
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                                 243 ACATCATGCGTGATATCATAGTGTCAATTTCTAGAGAGAAAATTTTGTCCACTTAGTAC 302
                                                                                                                                                                            303 AGAGTAATGGAAATAATGTAGCAGAGGAAAACTTCCGTCATGTTGCATACCATGACAGCA 362
                                                                                                                                                                                                                                                                        TGTGCCAAAAGGAAGCCATGGATTGGAGCATATTCGATCATTAACTTTTTTTACTGAGG 422
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae;
Brhartoideae; Oryzae; Oryza.

I (bases 1 to 808)
Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
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                                                                                                                   1343 TGGGAGATGGCTCTGATTTAGTTCAGGAAAACACTCGCCACATAGCATTCCATGGGAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATATCATCCGTGATATCACAGTTTCAATCTCGAGACAGGAAAATTTTGTATTGTTACCAA
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Unpublished (2004)
Contact: Rod A. Wing Arizona Genomics Institute
University of Arizona Rois Tracson, AZ 85721-0036, USA Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
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808 bp DNA linear GS6
OB Ba0047C05.r OB Ba Oryza brachyantha genomic clone
OB Ba0047C05 3', genomic survey sequence.
CL582275
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BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 145000 Std Brror: 0.00
Plate: 0047 row: C column: 05
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
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GSS.
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2 (contact: W. Richard McCombie, W.R. and Martienssen, R.A.

3 (contact: W. Richard McCombie

3 (bases denomic sequencing Center

4 (contact: W. Richard McCombie

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7 (contact: W. Richard McCombie

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                                                                                                                                                                                                     BZ338669 67-3 bp DNA linear GSS 06-NOV-2002 ia97a07.bl WGS-SbicolorF (JM107 adapted methyl filtered) Sorghum bicolor genomic clone ia97a07 5', genomic survey sequence.
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Pred. No. 4.5e-78;
0; Mismatches 197; Indels 12
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/db_xref="taxon:4558"
/clone="ia97a07"
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Matches 461; Conservative
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/dev_stage="mature"
/lab_host="DH10B"
/clone_lib="0B_Ba"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
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                                                                                           Length 808;
                                                                                         Query Match 10.7%; Score 320.2; DB 9; Length Best Local Similarity 64.3%; Pred. No. 7e-78; Matches 519; Conservative 0; Mismatches 273; Indels
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Search completed: February 13, 2005, 12:24:50 Job time : 6187.7 secs

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LENGTH: 3925 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECTLE TYPE: CDNA to mRNA
PEATURE:
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; LOCATION:
US-09-330-330-2
                                                                                                                                                          ,; Search time 326.59 Seconds (without alignments) 15015.533 Million cell updates/sec
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-864-680A-2

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| 157 Sequence 157, App Sequence 157, App Sequence 157, App Sequence 157, App Sequence 157, App Sequence 157, App Sequence 170, Appl Sequence 1, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 12896, A Sequence 17305, A Sequence 17305, A Sequence 17305, A Sequence 1833, Ap Sequence 183, Appl Sequence 14, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli | O BLAST DISEASE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
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| 2 US-08-310-912A<br>3 US-09-301-085-<br>3 US-09-004-838-<br>3 US-09-004-838-<br>3 US-09-004-838-<br>3 US-09-004-838-<br>2 US-08-588-983-<br>2 US-08-588-983-<br>4 US-09-588-983-<br>4 US-09-949-016-<br>4 US-09-949-016-<br>4 US-09-949-016-<br>4 US-09-949-016-<br>4 US-09-949-016-<br>4 US-09-004-838-<br>1 US-09-103-8403-<br>3 US-09-103-8403-<br>3 US-09-103-8403-<br>4 US-08-232-463-<br>3 US-09-103-8403-                                                                                                             | ALIGNMENTS  T. 1  -330-330-2  outnee 2, Application US/09330330  ent NO. 6274789  NERAL INFORMATION:  APPLICANT: Yano, Masahiro  APPLICANT: Yano, Masahiro  APPLICANT: Yano, Masahiro  APPLICANT: Yano, Masahiro  APPLICANT: Yano, Masahiro  APPLICANT: Yano, Masahiro  APPLICANT: Yano, Zi-Xuan  APPLICANT: Yano, Zi-Xuan  APPLICANT: Hang, Zi-Xuan  APPLICANT: Hang, Zi-Xuan  APPLICANT: Sasaki, Takuji  APPLICANT: Hang, Zi-Xuan  APPLICANT: Sasaki, Takuji  APPLICANT: Sasaki, Takuji  APPLICANT: Hang, Zi-Xuan  APPLICANT: Hang, Zi-Xuan  APPLICANT: Hang, Zi-Xuan  APPLICANT: Sasaki, Takuji  APPLICANT: Janis K.  APPLICATION NUMBER: JS, Janis K.  APPLICATION NUMBER: JS, Janis K.  REGISTRATION TIPERATION: JO. J. Janis K.  REGISTRATION NUMBER: 34,819  REGISTRATION INFORMATION:  NAME: Fraser, Ph.D., J.D., Janis K.  REGISTRATION NUMBER: 34,819  REGISTRATION INFORMATION:  TELEPHONE: 61/542-5070                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| 1.5 5134<br>1.5 5134<br>1.5 1662<br>1.5 4208<br>1.5 4208<br>1.5 3635<br>1.4 4 5195<br>1.3 4 451925<br>1.3 4 451925                                                                                                                                                                                                                                                                                                           | ALL SULT 1  -09-330-330-2 Sequence 2, Application US/09330330 Betent No. 6274789 GENERAL INFORMATION: APPLICANT: Yano, Masahiro APPLICANT: Yano, Masahiro APPLICANT: Saski, Takuji APPLICANT: Wango, Zi-Xuan APPLICANT: Wango, Zi-Xuan APPLICANT: Hannouchi, Utako APPLICANT: Hannouchi, Utako APPLICANT: Ishimaru, Lisa TITLB OF INVENTION: RICE GENE RE NUMBER OF SEQUENCES: 13 CORRESPONDENCE ADDRESS: ADDRESSEE: Fish & Richardson P STREET: 225 Franklin Street CITY: Boston STREET: AB COUNTRY: USA ZIP: 02110-2804 COMPUTER: READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: BESESO for Windows ' COMPUTER: BESESO for Windows ' SOFTWARE: Fastes of for Windows ' COMPUTER: 11-JUN-1999 PRILNG DATE: 11-JUN-1999 PRILNG DATE: 11-JUN-1999 PRILNG DATE: 11-JUN-1999 PRILNG DATE: 11-JUN-1999 PRILNG DATE: 11-JUN-1999 PRILNG DATE: 11-JUN-1999 PRILNG DATE: 12-JUN-1998 ATTORNEY/AGENT INFORMATION: NAME: FRESER NUMBER: 34,819 REGISTRATION INMBER: 34,819 REFERENCE/DOCKET NUMBER: 06501 TELEBOUNDER: 61/542-5070                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | RESULT 1 US-09-330-2 Sequence 2, Applement 2, Applement 1, Applement 2 APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: CORRESPONDE CORRESPONDE COMPUTER: COMPUTER: COMPUTER: APPLICATING SOFTWARE: CURRENT APPLICATING SOFTWARE: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG NAME: FILING DA ATTORNEY/AG ATTORNEY/AG ATTORNEY/AG ATTORNEY/AG ATTORNEY/AG ATTORNEY/AG ATTORNEY/A |

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1577 TGTTGTGCCACTTGAAATACTTGAGTATTGGATATTCGTCATCCATATATTCACTTCCCA 1636
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                                                                                                                                               CACTACCAAGTGAGATCAGTAAACTCCAATGTCTGCATACTCTTCGTTGTAGTAGAAA 1754
                                                                                                                                                                                  crrreccaaaaaccarcarcaaecrrcagaagcracagacarrcargcregegegeaa 2669
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APPLICANT: Sasaki, Takuji
APPLICANT: Sasaki, Takuji
APPLICANT: Wang, Zi-Xuan
APPLICANT: Yamonouchi, Utako
APPLICANT: Ishimaru, Lisa
TITLE OF INVENTION: RICE GENE RESISTANT TO BLAST DISEASE
TUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street CITY: Boston
                                                                                                                                                                                                                                                                                ; Sequence 3, Application US/09330330 ; Patent No. 6274789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8906
TELEFAX: 617/542-8906
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                      APPLICANT: Yano, Masahiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1103 TTGAAATCAAAAGGAATCGTCTAGTAGGTAGATGGATAGCAGAAGGGTTTGTTAGACCAA 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1163 AGGTTGGGATGACGACTAAGGATGTCGGAGAAGTTACTTTAATGAGCTAATCAACCGAA 1222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTATGATTCAACGAT-----CAAGAGTGGGCATAGCAGGAAAAATTAAGACTTGTCGAA 1276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCAFGATATCATCCGTGATATCACAGTTTCAATCTCGAGACAGGAAAATTTTGTATTGT 1336
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                                                                                                                    1832 TCTTGGCAAACCGACCAAAGACCCCAGAAGAGTGGAGAAATTGAACGAGAATTTCAATG 1891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2132 GCATGATTTTACCATTCCAGCAATCAGGTAGCAGGAAAATCAATTGACTCTTGCAAAG 2191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCCATGATCTCATGCGTGACATCGCCATCTCAAAGTCAACGGAGGAAAACCTTGTTTTTA 2251
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                                                                                                                                                                                                                                                                                 GCCGAATAATTGTGACTACAAGAAAAGAGAATATTGCCAACCATTGCTCAGGGAAAAATG 1651
                                                                                                                                                                                                                                                                                                                                                                                                                                 1712 AGGTÁTTTGAGGAGGCTACATATTTGGÁTGATCAGAÁCAÁTCCAGAGTTGGTTAAAGAAG 1771
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                                                                                           575 CTGAGTACCTGATAGAAGAGCTCAAGGAGAAGAGGTACTTTGTTGTTCTAGATGATCTAT 634
                                                                                                                                                                                                                                                                                                                      CACTGGTGTACCACCTTGATTTCTTGCAGATGAACGATGCCATAACATTGCTACTGAGAA 814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTGAACGAATTGTAAATAAATGTGGTCGTCTACCATTAGCAATACTTACAATAGGAGCTG 928
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                                                                                                                                                                     635 GGATTTTACATGGATTGGATAAATGAAATTGCATTTCCTAAGAACAATAAGAAGG 694
                                                                                                                                                                                                                                             GCAGTCAAATAGTAATAACCACTTGGAATGTTGATCTTGCGGAGAAGTGTGCCACAGGCCT 754
                                                        Gaps
                                                      18;
                 Length 3925;
                                                      Indels
                 Score 125.6; DB 3;
Pred. No. 2.1e-28;
0; Mismatches 629;
                   4.2%;
                                      Best Local Similarity Accountable Matches 551; Conservative
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APPLICANT: Valent, Bryan, Gregory
APPLICANT: Bryan, Gregory
APPLICANT: Bryan, Gregory
APPLICANT: Bryan, Gregory
TITLE OF INVENTION: A Pi-ta GENE CONFERRING DISEASE RESISTANCE TO PLANTS
FILE REPERRENCE: BB-1136
CURRENT FILING DATE: 1999-06-21
PRIOR PLING DATE: 1999-06-21
PRIOR APPLICATION NUMBER: 60/095229
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Microsoft Office 97
                                                           AGAATGGTGACCCTAGGTTACAACCACCTACCATCCCATCTGAAACCATGCTTTTTGTAT
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APPLICANT: Valent, Barbara S.
APPLICANT: Bryan, Gregory
APPLICANT: E. I. du Pont de Nemoura and Company
TITLE OF INVENTION: A Pi-ta GENE CONFERING DISEASE RESISTANCE TO PLANTS
FILE REPERENCE: BB-1136
CURRENT APPLICATION NUMBER: US/09/336,946B
CURRENT PILING DATE: 1999-06-21
PRIOR APPLICATION NUMBER: 60/095229
PRIOR FILING DATE: 1998-08-04
NUMBER OF SEQ ID NOS: 74
SOPTWARE: Microsoft Office 97
SEQ ID NO 68
LENGTH: 5222
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                                                                                                                                                                                                Length 5113;
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46.4%; Pred. No. 3.6e-13;
Live 0; Mismatches 341; Indels
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; Patent No. 6479731
; GENERAL INFORMATION:
                                                                                                                                                                                          Query Match
Best Local Similarity 46.4'
Matches 305; Conservative
; SEQ ID NO 3
; LENGTH: 5113
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-336-946B-3
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ORGANISM: Oryza sativa
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US-09-993-170-57
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; Sequence 57, Application US/0999170
; Patent No. 6743969
; GRNERAL INFORMATION:
APPLICANT: Valent, Barbara
; APPLICANT: Valent, Barbara
; TITLE OF INVENTION: Modification of a Plant Disease Resistance Gene
; TITLE OF INVENTION: Specificity and Method for Engineering Altered
; TITLE OF INVENTION: Specificity
; TITLE OF INVENTION: Specificity
; TITLE OF INVENTION: Specificity
; TITLE OF INVENTION: Specificity
; TITLE OF INVENTION: Specificity
; TITLE OF INVENTION: Specificity
; FILE REFERENCE: BB1385 US NA
; CURRENT APPLICATION NUMBER: 06/248,335
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Microsoft Office 97
; LENGTH: 5222
; TYPE: DNA
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                                                                                                  Gaps
                                                                                                  12;
                                                               Query Match
2.6%; Score 78.4; DB 4; Length 5222;
Best Local Similarity 46.4%; Pred. No. 3.7e-13;
Matches 305; Conservative 0; Mismatches 341; Indels 12
 ; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-336-946B-68
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APPLICANT: Valent, Gregory

TITLE OF INVENTION: Modification of a Plant Disease Resistance Gene
TITLE OF INVENTION: Modification of a Plant Disease Resistance Gene
TITLE OF INVENTION: Specificity and Method for Engineering Altered
TITLE OF INVENTION: Specificity
FILE REPERENCE: BB1385 US NA
CURRENT APPLICATION NUMBER: US/09/993,170
CURRENT FILING DATE: 2001-11-26
PRIOR PAPLICATION NUMBER: 60/248,335
PRIOR PAPLICATION NUMBER: 60/248,335
PRIOR PAPLICATION NUMBER: 60/248,335
PRIOR PAPLICATION NUMBER: 60/248,335
SPECOFUNATE: Microsoft Office 97
SEQ ID NO 60
LENGTH: 5696
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                                                                                 Gaps
                                                                             12;
Length 5222;
Score 78.4; DB 4; Length 5
Pred. No. 3.7e-13;
0; Mismatches 341; Indels
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Query Match 2.6%;
Best Local Similarity 46.4%;
Matches 305; Conservative
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APPLICANT: Valent, Barbara S.
APPLICANT: Valent, Barbara S.
APPLICANT: STAIN, Gregory
APPLICANT: E. I. du Pont de Nemours and Company
TITLE OF INVENTION: A Pi-ta GENE CONFERRING DISEASE RESISTANCE TO PLANTS
TILE REFERENCE: BB-1136
CURRENT FILING DATE: 1999-06-21
PRIOR APPLICATION NUMBER: 60/095229
PRIOR RILING DATE: 1998-08-04
NUMBER OF SEQ ID NOS: 74
SOPTWARE: MICROSOFT OFFICE 97
SEQ ID NO
                                                                                                                             683 ACANTAAGAAGGCCAGTCAAATAGTAATAACCACTTGGAATGTTGATCTTGCGGAGAAGT
                                                                                               12;
               , OTHER INFORMATION: Description of Artificial Sequence:Chimeric US-09-993-170-60
                                                              Length 5696;
                                                           Score 78.4; DB 4; Length 56
Pred. No. 3.9e-13;
0; Mismatches 341; Indels
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                                                              2.68;
                                                                              Best Local Similarity 46.4
Matches 305; Conservative
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TYPE: DNA
ORGANISM: Oryza Bativa
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Sequence 56, Application US/09993170

Sequence No. 6743969

GENERAL INFORMATION:

APPLICANT: Valent, Barbara

TITLE OF INVENTION: Specificity and Method for Engineering Altered

TITLE OF INVENTION: Specificity

TITLE OF INVENTION: Specificity

TITLE OF INVENTION: Specificity

CURRENT FILING DATE: 2001-11-26

PRIOR APPLICATION NUMBER: US/09/993,170

PRIOR APPLICATION NUMBER: 60/248,335

PRIOR FILING DATE: 2000-11-14

NUMBER OF SEQ ID NOS: 60

SOFTWARE: Microsoft Office 97

LENGTH: 5757
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                                                                 Gaps
Score 78.4; DB 4; Length 5757;
Pred. No. 4e-13;
0; Mismatches 341; Indels 12;
      2.6%;
                                     46.48;
   Query Match
Best Local Similarity 46.43
Matches 305; Conservative
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ORGANISM: Oryza sativa
US-09-993-170-56
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Query Match
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                                                    12;
              2.6%; Score 78.4; DB 4; Length 5757;
46.4%; Pred. No. 4e-13;
tive 0; Mismatches 341; Indels 12
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TITLE OF INVENTION: Bs2 Resistance Gene
FILE REFERENCE: 50687
CURRENT APPLICATION NUMBER: US/09/360,186
CURRENT FILING DATE: 1999-07-23
EARLIER APPLICATION NUMBER: 60/093,957
EARLIER FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO SEQ ID NOS: 9
LENGTH: 2718
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Patent No. 6262343
GENERAL INFORMATION:
                                 Best Local Similarity 46.4
Matches 305; Conservative
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; LOCATION: (1)..(2718)
US-09-360-186-4
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  Length 2718;
                                                      0; Mismatches 285; Indels
2.0%; Score 61; DB 3;
17.1%; Pred. No. 8e-08;
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APPLICANT: Tal, Thomas H
TILE OF INVENTION: B82 RESISTANCE GENE
FILE REFERENCE: 42250/234021 (5830-4A)
CURRENT APPLICATION NUMBER: US/09/864,680A
CURRENT FILING DATE: 1999-07-23
PRIOR APPLICATION NUMBER: US 09/360,186
PRIOR APPLICATION NUMBER: US 09/360,186
PRIOR APPLICATION NUMBER: US 06/093,957
PRIOR PILING DATE: 1998-07-23
PRIOR FILING DATE: 1998-07-23
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                         47.18;
                                                      Matches 264; Conservative
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US-09-864-680A-4
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SOFTWARE: PatentIn versi
                            Similarity
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LENGTH: 2718
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2.0%; Score 61; DB 4; Length 309
Best Local Similarity 47.1%; Pred. No. 9e-08;
Matches 264; Conservative 0; Mismatches 285; Indels
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Patent No. 676295
GENERAL INFORMATION
APPLICANT: Staskawicz, Brian J
APPLICANT: Tai, Thomas H
TILE OF INVENTION: B92 RESISTANCE GENE
TILE REFERENCE: 42250/234021 (5830-4A)
CURRENT APPLICATION NUMBER: US/09/864,680A
CURRENT FILING DATE: 2001-05-24
PRIOR FILING DATE: 1999-07-23
PRIOR FILING DATE: 1999-07-23
PRIOR FILING DATE: 1998-07-23
PRIOR FILING DATE: 1998-07-23
NUMBER: OF SEG ID NOS: 14
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LOCATION: (93)..(2810)
OTHER INFORMATION:
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US-09-864-680A-2
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US-09-864-680A-2
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                                                       755 raaadadaadaddacriraaridicriddardarariciddagrigraagrorddaig 814
        TCAAGGAGAAGAGGTACTTTGTTGTTCTAGATGATCTATGGATTTTACATGATTGGAATT
                                                                                                           GGATAAATGAAATTGCATTTCCTAAGAACAATAAGAAGGGCAGTCAAATAGTAATAACCA
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47.1%; Pred. No. 9e-08;
tive 0; Mismatches 285; Indels
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SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 2
LENGTH: 3099
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Matches 264; Conservative
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; LOCATION: (93)..(2810)
US-09-360-186-2
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                                                                                                                                                                                                                             GGTTACCACTAACTATTGTCGTGGTTGCAGGGCTTCTCAAATCTAAAAGGACAATAGAAG 2581
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Pred. No. 6.1e-07;
0; Mismatches 285; Indels 12; Gaps
APPLICANT: Staskawicz, Brian J
APPLICANT: Bahlbeck, Douglas
APPLICANT: Tai, Thomas H
TITLE OF INVENTION: BS2 RESISTANCE GENE
FILE REFERENCE: 42250/234021 (5830-4A)
CURRENT APPLICATION NUMBER: US/09/864,680A
CURRENT FILING DATE: 1099-07-23
PRIOR APPLICATION NUMBER: US 60/093,957
PRIOR FILING DATE: 1999-07-23
PRIOR FILING DATE: 1999-07-23
PRIOR FILING DATE: 1998-07-23
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGATAGCAGAAGGGTTTGTTA 1156
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Best Local Similarity 47.1%;
Matches 264; Conservative
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                                                                                                                                                                                                                                                                                                                            ----AGCATTACCATATGAGTTCGAGACTGTTGGAAAGCAAATCGCAGATGAATGTCACG 1134
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  CTTGGAATGTTGATCTTGCGGAGAAGTGTGCCACAGCCTCACTGGTGTACCACCTTGATT 775
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Pred. No. 6.1e-07;
0; Mismatches 285; Indels 1:
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Patent No. 626243

GENERAL INFORMATION:
APPLICANT: Staskawicz, et al.
TILE REFERENCE: 50687

CURRENT APLICATION WUMBER: US/09/360,186

CURRENT APLICATION NUMBER: 60/093,957

EARLIER APLICATION NUMBER: 60/093,957

EARLIER PILING DATE: 1999-07-23

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1

LENGTH: 31491
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Best Local Similarity 47.1%;
Matches 264; Conservative
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US-09-360-186-1
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US-09-360-186-1
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2466 ----AGCATTACCATATGAGTTCGAGACTGTTGGAAAGCAAATCGCAGATGAATGTCACG 2521
                                                                                                                2522 GGTTACCACTAACTATTGTCGTGGTTGCAGGGCTTCTCAAATCTAAAAGGACAATAGAAG 2581
                                                                                                                                                                                                             2582 ATTGGAAAACTGTTGCTAAAGATGTCAAGTCATTCGTCACAAATGATCCTGATGAACGAT 2641
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                                                                          GTCTACCATTAGCAATACTTACAATAGGAGCTGTGCTTGCAACTAAACAGGTGTCAGAAT 955
                                                                                                                                                             956 GGGAGAAATTCTATGAACACCTTCCTTCAGAACTAGAAATAAACCCAAGCCTGGAAGCTT
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APPLICANT: Williamson, Valerie M.
APPLICANT: Williamson, Isgouhi
APPLICANT: Yaghoobi, Jafar
APPLICANT: Bodeau, John
APPLICANT: Bodeau, John
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Pest Resistance in Plants
NUMBER OF SEQUENCES: 5
CORRESPONDENCES: ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth, Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/947,823
FILING DATE: 09-0CT-1997
CLASSIFICATION B00
PRIOR APPLICATION BATA:
APPLICATION NUMBER: US/08/947,823
FILING DATE: 09-0CT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05-0CT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,191
APPLICATION NUMBER: US 60/028,191
APPLICATION NUMBER: US 60/028,191
APPLICATION NUMBER: US 60/028,191
APPLICATION NUMBER: US 60/028,191
APPLICATION NUMBER: US 60/028,191
APPLICATION NUMBER: US 60/028,191
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REGISTRATION NUMBER: 34,774
REPERENCE/DOCKET NUMBER: 023070-070210US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                           1136 GGATAGCAGAAGGGTTTGTTA 1156
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-08-947-823-2
; Sequence 2, Application US/08947823
; Patent No. 6114605
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TYPE: nucleic acid
STRANDEDNESS: single
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CITY: San Francisco
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                               Gaps
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9
                                                                                                                                                                                          Length 3997;
LOCATION: 85.3852
CTHER INFORMATION: /note= "Copy 1 cDNA for M1 nematode /noter information: resistance gene of tomato" US-08-947-823-2
                                                                                                                                                                                          1 Similarity 51.0%; Score 59; DB 3; Length 399 Similarity 51.8%; Pred. No. 4.8e-07; Conservative 0; Mismatches 145; Indele
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ne : 335.59 secs
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                                                                                                                                                                                          Query Match
Best Local Similarity 51.8
Matches 162; Conservative
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Sequence Sequence Sequence Sequence

Sequence 1, Appl 1, Sequence 49433, A Sequence 6, Appl 1, Sequence 86, Appl 1, Sequence 97, Appl 1, Sequence 97, Appl 1, Sequence 94, Appl 1, Sequence 910, Appl 1, Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 11019, A Sequence 1

Scoring table:

Searched:

Perfect score:

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Minimum DB Maximum DB

Database

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GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE REFERENCE: 035718/525062
CURRENT APPLICATION NUMBER: US/10/656,394A
CURRENT FILING DATE: 2003-09-05
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 2997
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Best Local Similarity 100.0
Matches 2997; Conservative
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ORGANISM: Oryza minuta
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Sequence 34053, Sequence 51200, Sequence 98981,

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Score

Result No.

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Gaps

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| 121 TTGTTTAGACATGGTGTTGGACGGTCGAATGGTGGGCCTGTTGTAGGTATGGTGGTGGTGCTT 180 | CGAAATGTGGATGAAGCTGAGGTTTTCTGACTCCAAGAAAAGGCTGGTTGAAAAGGCTGGTTGAAATGTGGAATGAGGTTGATGAATTTCTGACTCCAAGAAAAGGCTGGTTGAAATGTGGAATGAAAGGTGAGGTTTTCTGACTCCAAGAAAAGGCTGCTTGAAATGGTTGAAAAGGCTGCTTGAAATGCTAGAAAAGGCTAGAAAAGGTTTTCTGACTCCAAGAAAAGGCTTGGAAAAGGTTTTCTGACTTGAAAAAGGCTTGAAAAAGGTTTTCTGAAAAAGGTAAAAGGTTGAAAAAAGGTTTTCTAAAAAAGGTTAAAAAAAGGTAAAAAAAA | 301 ATGATCGATACCTAATGATGGTCCGGCCAAGGTAATCTGTGTTGGTGGTGGGGT 350 361 GGTTTAGGCAAGACACTCTTTCGAGGAAGATCTTTGAAAGCGAAGAAGACTAAGGAAG 420 361 GGTTTAGGCAAGACACTCTTTCGAGGAAGATCTTTGAAAGCGAAGAAGATAAGGAAG 420 AACTTCCCTTGCAAGACATCTTCAAAAGATTTAACAGAAGCTAAGAAGAAAAATCATTAAGAAAGA                                                                                    | 421 AACTICCCTIGCAATGCTTGGATTACAGTGTCACAATCATTTCACAGGATTGAGCTACTT 480  481 AAAGATATGATACACCAACTTCTTGGCCCCAGTTCTCTGGAATACAAGAATTG 540  481 AAAGATATGATACGCCAACTTCTTGGCCCCAGTTCTTCTGGAATTGCAAGAATTG 540  541 CAAGGGAAGGTGGTGGTGAATACATCATCTTTCTGAATACATAC                                               | 541 CAAGGGAAGGTGGTGGTGGTACATCATCTTTCTGGTACCTGTATAGAAGGGCTCAAG 600 601 GAGAAGAGGTACTTGTTGTTCTAGATGATTGTATTTTACATGATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATGGAATTGGAATTGGAATGGAATGGAATTGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGA | 661 AATGAAATTGCATTTCCTAAGAACAATAAGAAGGGCAGTCAAATAACAATAACCACTTGG 720                                      | CAGATGAACGATGCCATAACATTGCTACTGGAAAAACAAATAAAAATCATGAAGACATG CAGATGAACGATGCCATAACATTGCTACTGGAAAAACAAATAAAAATCATGAAGACATG CAGATGAACGATGCCATAACATTGCTACTGGAAAAACAAATATGTAAAAATATGCTACTGGAAAAAAAA |                                                                                                                                                                                                            | 961 AAATTCTATGAACACCTTCCTTCAGAACTAGAATAAACCCAAGCCTGGAAGCTTTGAGG 1020  | 1021 AGATGGTGACCCTAGGTTACAACCACCTCCCATCTGAACCATGCTTTTTGTAT 1080 1081 CTAAGTATCTTTCCTGAGGATTTTGAAATCAAAGGAATGGTCTGGTGAGGTAGGT | GCAGAAGGGTTTGTTAGACCAAAGGTTGGGATGACGACTAAGGATGTCGAGAAAGTTAC<br>      |

| Query Match         80.4%;         Score 2408.6;         DB 18;         Length 4596;           Best Local Similarity         96.1%;         Pred. No. 0;         1           Matches 2481;         Conservative         0;         Mismatches         99;         Indels         3;         Gaps         1;           Qy         169         ATGGTGGCATCTGGCAACCAGTCATGCTTAGCAATAGATTCCTATGCAGAAAA         228         ATGGTGGCATCTGGCAACCAGTCAACGAATGAGCTGAGC | 289 AGCCTGCTTGAAATGATCGATACCAATGCTAATGATGGTCCGGCCAAGGTAATCTGTGTT    | 30<br>30<br>36                                   | 529 TIGCAAGATIGCAAGGAAGGIGGTGGTCCAAGTACATCATCTTCTGAGTACCTGATA                                                                                                                                                                                                                         | Qy         649 TGGAATTGGATAAATGAAATTGCATTTCCTAAGAACAATAAGAGGCAGTCAAATAGTA 708           D         1 | Qy         769 CTTGATTTCTTGCAGATGAAGCATGCCATAACATTGCTACTGAGAAAAAAAT 828           Db         (01 [1] [1] [1] [1] [1] [1] [1] [1] [1] [1                            |                                                                                                                                                                                                                                                                                                       |                                                                                                                                                                                                                                                                                                       |
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| Db   2281 TTATTGAGGAGGAAACTAAAGGAAAGCTAGCTGATACTTGGGGCATTGCCCAAC 2340                                                                                                                                                                                                                                                                                                                                                                                          | Db   2461 AGATTTGAGGACGCAGCTCGCCCAGTTGGAAAAGATCAGATTCTGCAGGTTG 2520 | 2641 CCCGTGCTGCGAAGGGGGGGGCCGAAGTGACCGACCTTGCTTG | Oy         2761         CGAAGAGATAAGCACAGCTCAAGCTGATTTATCAAGTGATCTCCTCCTCCATTGGC         2820           Db         2761         CGAAGAGATAAGCACAGCTCAAGCTGGTTTTATCAAGTGATGATCTCCTCCTCCATTGGC         2820           Oy         2821         ATCTCCGGTCGCTCCTCTCTGCGCTGCTCTCTGCGCTGCTG | Oy         2881 GATCTAAGGGGGCTTCCACTTTCTTCAATTGCGTCTCAGGCTCTCCGATTCTTCCCTCTCG         2940          | SULT 2<br>-10-437-963-37316<br>Sequence 37316, Application US/10437963<br>Publication No. US20040123343A1<br>GENERAL INFORMATION:<br>APPLICANT: La Rosa, Thomas J. | APPLICANT: Zhou, Yihua  APPLICANT: Cao, Yongwei  APPLICANT: Wu, Wei  APPLICANT: Wu, Wei  APPLICANT: Barbaruk, Brad  APPLICANT: Barbaruk, Brad  TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement | ; FILE REFERENCE: 38-21(53221)B ; CURRENT APPLICATION NUMBER: US/10/437,963 ; CURRENT FILING DATE: 2003-05-14 ; NUMBER OF EEG ID NOS: 204966 ; SEQ ID NO 37316 ; LENGTH: 4596 ; TYPE: DNA ; ORGANISM: Oryza Bativa ; FEATURE: ; CTHER INFORMATION: Clone ID: PAT_MRT4530_41056C.1 US-10-437-963-37316 |

|                                                    | WESULT   WESULT   WESULT   WESULT   WESULT   WESULT   WESULT   WESULT   WESULT   WESULT   WESULT   WESULT   WESULT   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATION   WESUNDATI |
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| 189   GGAGAAAGTTACTTTAATGAGCTAATCAACCGAAGTATCAATCA | 1729 CTGCATACTCTTCGTTGTAGAAAGTTTCTTTCTGACAACTTTAGTCTAAACCACCCA 1788  1561 CTGCATACTCTTCGTTGTAGAAAGTTTCTTTATGACACTTAGTCTAAACCACCCA 1620  1789 ATGAAGTGCATAACACAATAGCCTGCCTAAAGTTTCACCTTAGTTAG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |

| Db 1627 ATGTCCTGCAAAACAGGATTGGATTGGAGCATTATTCGATCATTAGTTTTTTGGTGAC 1686 | OY 1462 AGACCCAAGAGTCTAGCACATGCAGTTTGTCCAGATCAATTGAGGATGTTACGGGTCTTG 1521 | OY 1522 GATCTTGAAGATGTGACATTCTTAATCACTCAAAAAGATTTCGACCGTATTGCATTGTTG 1581                 | OY 1582 TGCCACTTGAAATACTTGAGTATTGGATATTCGTCATATATTCACTTCCCAGATCC 1641                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 1642 ATTGGTAAACTACAGGCCTACAAACTTTGAACATGCCGAGCACTACATTGCAGCACTA [ | Oy 1702 CCAAGTGAGATCAGTAAACTCCAATGTCTGCATACTCTTCGTTGTAGAAAGTTTGTT 1761<br> | OY 1762 TCTGACAACTTTAGTCTAAACCACCCAATGAAGTGCATAACTAAC | OY 1822 AAAGTATTCACACCTTTAGTTGGCGATGATCGGCAATACAAATTGCTGAATTGCAC 1881 | Qy 1882 ATGGCCACCAAAAGTTGCTGGTATAAATCATTCGGTGTGAAGGTACCCAAAGGAATAGGT 1941 | OY 1942 AAGTTGCGAGACTTACAGGTTCTAGAGTATGTAGATATCAGGCGGACCAGTAGTAGAGCA 2001 | 2002 ATCAAAGAGCTGGGGCAGTTAAGCAAGCTGAGGAAATTAGGTGTGATGACAAATGGCTCG 2061 | 2062 | 2122 CTCTATGTGAATGCTGGAGAATCTCAGATGGTGGAACACTTGAGTGCCTAGATTCTATT 2181 2147 CTCTATGTGAATGCTGCGTTATTATCAGATATTGAAACACTTGAGTGCCTAGATTCTATT 2406 | 2182 | 2242 AACTGGATTGAGCAGCTCACCTGAAGAAGATCTACTTATTGAGGAGCAAACTAAAG 2301 2467 AACTGGATTGAGCAGCTCACCTGAAGAAGATCTACTTATTGAGGAGCAAACTAAAG 2526 | 2302 GAAGGTAAAACCATGCTGATACTTGGGGCATTGCCCAACCTCATGGTCCTTGATCTTTAT 2361 | 2362 CGGAAAGCTTACCTTGGGGAGAAGCTAGTÀTTCAAAACAGGAGCATTCCCAAATCTTAGA 2421<br>                                                                                                                 | 2422 ACACTTTCGATTTACGATTTGGATCAGCTAAGAGAGATTAGATTTGAGGACGGCAGCTCG 2481 | / 2482 CCCCAGTTGGAAAAGATAGAAATCAGATTCTGCAGGTTGGAATCAGGGATTATTGGTATT 2541 |
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| 322 GATGGTCCGGCCAAGGTAATCTGTGTTGGGATGGGTGGTTTAGGCAAGACAGCTCTT<br>       | TCGAGGAAGATCTTTGAAAGCGAAGAGACATTAGGAAGAACTTCCCTTGCAATG                    | ATTACAGTGTCACAATCATTTCACAGGATTGAGCTACTTAAAGATATGATGCGCATTAAAGATGTTAAAGATATGATTGAGCAATCAAT | CTTGGCCCCCGGTTCTCTGGATCACTCTTGCAAGAATTGCAAGGGAAGGTGGTGCTGCAAGGCCCGGTTCTCTGGAAGGTGTGCAAGAATTGCAAGAAAGGGAAAGTGGTTGCTAGCAAGAAATTGCAAGAAAGGGAAAGTGGTTGCTAAGAAGGTGGTGGTTGCTAAGAAATTGCAAGAAAGGGAAAATTGCAAGAAAGTGAAGAAGGTGGTTGCTAAGAAATTGCAAGAAAATTGCAAGAAAATTGCAAGAAAATTGCAAGAAAATTGCAAGAAAATTGCAAGAAAATTGCAAGAAAATTGCAAGAAAATTGCAAGAAAATTGCAAGAAAATTGCAAGAAAATTGCAAGAAAATTGCAAGAAAAATTGCAAGAAAAATTGCAAGAAAAATTGCAAGAAAAATTGCAAGAAAAATTGCAAGAAAAATTGCAAGAAAAATTGCAAGAAAAATTGCAAGAAAAATTGCAAGAAAAATTGCAAGAAAAATTGCAAGAAAAATTGCAAGAAAAATTGCAAGAAAAATTGCAAGAAAAATTGCAAGAAAATTGCAAGAAAATTGCAAGAAAATTGCAAGAAAAATTGCAAGAAAAATTGCAAGAAAATTGCAAGAAAATTGCAAGAAAATTGCAAGAAAAATTGCAAGAAAAATTGCAAGAAAAATTGCAAGAAAAATTGCAAGAAAAATTGCAAGAAAAATTGCAAGAAAAATTGCAAGAAAAATTGCAAGAAAAATTGCAAGAAAAATTGCAAGAAAAATTGCAAGAAAATTGCAAGAAAAATTGCAAGAAAAATTGCAAGAAAAATTGCAAGAAAAATTGCAAGAAAAATTGCAAGAAAAATTGCAAGAAAATTGCAAGAAAATTGCAAGAAAATTGCAAGAAAAATTGCAAGAAAATTGCAAGAAAATTGCAAGAAAATTGCAAGAAAATTGCAAGAAAATTGCAAGAAAATTGCAAGAAAATTGCAAGAAAATTGCAAGAAAATTGCAAGAAAATTGCAAGAAAATTGCAAGAAAATTGCAAAAATTGCAAGAAAATTGCAAGAAAATTGCAAGAAAATTGCAAGAAAATTGCAAGAAAATTGCAAGAAAATTGCAAAGAAATTGCAAGAAAATTGCAAGAAAATTGCAAGAAAATTGCAAAATTGCAAGAAAATTGCAAGAAAATTGCAAAAATTGCAAAATTGCAAGAAAATTGCAAGAAAATTGCAAAAATTGCAAAGAAATTGCAAAAATTGCAAAAATTGCAAAAATTGCAAAAATTGCAAAAATTGCAAAAATTGCAAAAATTGCAAAAATTGCAAAAATTGCAAAAATTGCAAAAATTGCAAAAATTGCAAAAATTGCAAAAATTGCAAAAATTGCAAAAATTGCAAAAATTGCAAAAATTGCAAAAATTGCAAAAATTGCAAAAATTGCAAAAATTGCAAAAATTGCAAAAATTGCAAAAATTGCAAAAATTGCAAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAAATTGAAAATTGAAAAATTGAAAATTGAAAAATTGAAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTAAAATTAAAAATTGAAAAATTAAAAATTAAAATTAAAAATTAAAATTAAAATTAAAA |                                                                   | 622 CTAGATGATCTATGGATTTTACATGATTTGGAATTGGATAAATGGAATTTGCATTTCCTAAG<br>     |                                                       | 742 TGTGCCACAGCCTCACTGGTGTACCACCTTGATTTCTTGCAGATGAACGATGCCATAACA      |                                                                           |                                                                           |                                                                        |      | 1042 AACCACCTACCATCTGAAACCATGCTTTTTGTATCTAAGTATCTTCCTGAGGAT<br>                                                                              |      | AAGGTTCGGATGACGACTAAGGATGTCGGACAAAGTTACTTTAATGAGCTAATC<br>                                                                            |                                                                        | GATATCATCGGGATATCACAGTTTCAATCTCGAGACAAATTTTGTATTGG  GATATCATCGGGAAAATTTTGAATCTCGAGACAAAATTTTGTATTGG  GATATCATCGGAAAATTTTGAATCTCAAGACAAAATTTTGTATTGG  GATATCATCCGAAAAATTTTGAATCTCAAAAAAAAAA |                                                                        | 156/ ATGECTGCAAAACAGGATTGGATTGGAGAAAACACTCGCCACATAGCATTCCATGGGAGT        |

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Publication No. US20040006788A1
GENERAL INFORMATION:
APPLICANT: Wang, Guo-liang
APPLICANT: Liu, Guife
APPLICANT: Liu, Guife
APPLICANT: Liu, Guife
APPLICANT: Liu, Guife
TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pla
FILE REFERENCE: 22727/04108
FILE REFERENCE: 22727/04108
FILE REFERENCE: 2021-27
FILE REPERENCE: 2003-01-27
FRIOR APPLICATION NUMBER: 60/352,106
FRIOR FILING DATE: 2002-01-25
FRIOR FILING DATE: 2002-01-25
SOFTWARE: Patentin version 3.1
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Best Local Similarity 96.4%;
Matches 2456; Conservative
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Query Match 79.9%; Score 2395.2; Best Local Similarity 96.2%; Pred. No. 0; Matches 2454; Conservative 0; Mismatches
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                                                                                                                                       FEATURE:
NAME/KEY: misc_feature
LOCATION: 23216
OTHER INFORMATION: n = A,T,C
                                                                                                                     TYPE: DNA
ORGANISM: Oryza minuta
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                 ATCAAAGAGCTGGGGCCAGTTAAGCAAGCTGAGGAAATTAGGTGTGATGACAAATGGCTCG
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Sequence 13, Application US/10656394A
Publication No. US20040210957A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: Cloning and Characterization of the
TITLE OF INVENTION: Droad-spectrum resistance gene Pi2
TITLE REFERENCE: 035719/525062
CURRENT APPLICATION NUMBER: US/10/656,394A
CURRENT FILING DATE: 2003-09-05
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 99090
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                                      GGTCGACAAAGGAAAAATGTAAGATACTTTATGCAGCCATTGAGAAGCTCTCTTCCCTCC
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; Publication No. US20040210957A1
; GENERAL INFORMATION:
; APPLICANT: Wang et al.
; TITLE OF INVENTION: Cloning and Characterization of the
; TITLE OF INVENTION: Droad-spectrum resistance gene Piz
; TITLE OF INVENTION: Droad-spectrum resistance gene Piz
; TITLE OF INVENTION: Droad-spectrum resistance gene Piz
; CURRENT APPLICATION UNMER: US/10/656,394A
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 3099
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; ORGANISM: Oryza m:
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...('US-10-656-394A-7
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                CAATAGGAGCTGTGCTTGCAACTAAACAGGGTGTCAGAATGGGAGAAAATTCTATGAACACC
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                                                        TTCCTTCAGAACTAGAAATAAACCCAAGCCTGGAAGCTTTGAGGAGAATGGTGACCCTAG
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TACCAATGGGAGATGGCTCTGATTTAGTTCAGGAAACACTCGCCACATAGCATTCCATG GTGACAGACCCAAGAGTCTAGCACATGCAGTTTGTCCAGATCAATTGAGGATGTTACGGG GAGCAATCAAAGAGCTGGGGCAGTTAAGCAAGCTGAGGAAATTAGGTGTGATGACAAATG TGCCTAACTGGATTGAGCAGCTCACCTGAAGAAGATCTACTTATTGAGGAGCAAAC GGAGTATGTCCTGCAAAACAGGATTGGATTGATTGATTTTTG GGAGTATGTCCTGCAAAACTGGATTGGATTGGAGCATTATTCGATCATTAGCTATTTTTG TGCCTAAAGTATTCACACCTTTAGTTAGTCGCGATGATCGTGCAATACAAATTGCTGAAT 2297 TAAAGGAAGGTAAAACCATGCTGATACTTGGGGCATTGCCCAACCTCATGGTCCTTGATC GTGACAGACCCAAGAGTCTAGCACATGCAGTTTGTCCAGATCAATTGAGGATGTTACGGG TIGITICIGACAACTITAGICTAAACCACCAAIGAAGIGCATAACITAACACAATAIGCC TICATTATGACAACTITAGICTAAACCACCCAATGAAGTGCATAACTAACACAATATGCC 1937 TAGGTAAGTTGCGAGACTTACAGGTTCTAGAGTATGTAGATATCAGGCGGACCAGTAGTA 

| 317 CTCTTTCGAGGAAGATCTTTGAAAGCGAAGAAGACATTAGGAAGAACTTCCCTTGCAATG 436                                                                                                                                                                                                     | TIGITCTAGATGATCTATGGATTTACATGATGGATTAGATGATTTC 676 | L 0 L 0                                                                                                                                                                                                                                                                                    |                                                                                                                                                                                                                                                                                                                                                                                | GTTACAACCACCTACCATCCCATCTGAAACCATGCTTTTTGTATCTTAAGTATCTTTCTG                                                                                                                                  | 1 6 1 6             | FIGH 133 FIGH 173 FIGH 173 CATG 139 CATG 139 FITTG 145 FITTG 185 FITTG 185 |
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| Db 2522 TAAAGGAAGGTAAAACCATGCTGATACTTGGGGCACTGCCCAACCTCATGTCTCATC 2581  Qy 2357 TTTATCGGAAAGCTTACCTTGGGGAAGCTTACTTCAAAACAGGACATTCCCAAATC 2416  Db 2582 TTTATCGGAAAGCTTACCTTGGGGAAAGCTAGTTTCAAAACAGGAGCATTCCCAAATC 2416  Qy 2417 TTAGAACACTTTACGATTACGATAGATTTGAAAAAAAAAA |                                                    | Qy         2657 GGGAGGACCGAAGTGATCACGACCTTGTGACGCCGAAGGATCCCTGTTGAAGTGG         2716           Db         2882 ACAGTGACGAAGGATCTCTATAGAAGTGC         2941           Qy         2717 AAGAACGGAACGAAGGAGGAGGA         2748           Db         2942 AAACAGGATCCTCCCTGCAAGGAGGA         2973 | RESULT 7 US-10-352-179-92 ; Sequence 92, Application US/10352179 ; Publication No. US20040006788A1 ; GENERAL INFORMATION: ; APPLICANT: Wang, Guo-liang ; APPLICANT: Wang, Guo-liang ; APPLICANT: Liu, Guifu ; TITLE OF INVENTION: Proceedures and Materials for Conferring Disease Resistance in Pla ; FILE REFERENCE: 22727/04108 ; CURRENT APPLICATION NUMBER: US/10/352,179 | PRIOR PRICATION NUMBER: 60/322,106  PRIOR FILING DATE: 2002-01-25  NUMBER OF SEQ ID NOS: 97  SOFTWARE: Patentin version 3.1  SEQ ID NO 92  IENGTH: 3276  TERGAN: 3276  ORGANISM: Oryza minuta | <pre>prature:</pre> | 9 NTN NTN 9_9                                                              |

    

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                                                                                                                                 Length
                                                                                                                               Score 2359.8; DB 18; Lengt
Pred. No. 0;
0; Mismatches 117; Indels
APPLICANT: Wang et al.
TITLE OF INVENTION: Cloning and Characterization of TITLE OF INVENTION: broad-spectrum resistance gene 1 FILE REFERENCE: 035718/252662
CURRENT APPLICATION NUMBER: US/10/656,394A
CURRENT FILING DATE: 2003-09-05
SOFTWARE FALESQ for Windows Version 4.0
SEQ ID NO 16
                                                                                                                               78.7%;
95.4%;
                                                                                                                                                 Conservative
                                                                                          TYPE: DNA
CORGANISM: Oryza minuta
US-10-656-394A-16
                                                                                                                              Query Match
Best Local Similarity
Matches 2430; Conserv
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Pred. No. 0;
0; Mismatches
Best Local Similarity 77.1%;
Matches 2163; Conservative
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Schonce 2483, Application US/10437963

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GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 30-21(5322)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NO 2482
SRO ID NOS: 204966
SSO ID NOS: 204966
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ORGANISM: Oryza sativa
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US-10-352-179-90

Sequence 90, Application US/10352179

Sequence 90, Application US/10352179

Sequence 90, Application US/10352179

Sequence 90, Application US/10352179

Publication No. US20040006788A1

GENERAL INFORMATION:

APPLICANT: Warg, Guo-liang

TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pla

TILE REPRENCE: 22727/04108

CURRENT APPLICATION NUMBER: US/10/352,179

CURRENT FILING DATE: 2002-01-25

NUMBER OF SEQ ID NOS: 97

SEQ ID NO 90

LENGTH: 3220
                          CIGCTITGICITICACTIGATGCITACCTCGGGGGGGAAATCTAGIATICAGAACAGGAGCA
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Best Local Similarity 74.1%; Pred. No. 0;
Matches 1893; Conservative 0; Mismatches 620;
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; ORGANISM: Oryza minuta
US-10-352-179-90
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CAGCTTCCTTCAGAACTTGAAAGCAACCCAAGCCTTCAAGCTTTGAGGAGAATGGTGACC 1257
                                      CTTGGCTACAACCACCTGCCATCTCATCTGAAATCATGCTTTTTTGTACCTAAGTATCTTC
                                                                        TACATTGCAGCACTACCAAGTGAGATCAGTAAACTCCAATGTCTGCATACTCTTCGTTGT
                     CTAGGTTACAACCACCTACCATCCCATCTGAAACCATGCTTTTTGTATCTAAGTATCTTT
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| 1554 AAAAGATTTCGACCGTATTGCATTGTTGCCCACTTGAAATACTTGAGTATTCGATATTC              | 1614 GTCATCCATATATTCACTTCCCAGATCCATTGGTAAACTACGGGGCCTACAACTTTGAA 361 GTCATCCATATATTCACTTCCAGATCCATTGGTAAACTACAGGGCCTACAACTTTGAA 361 GTCATCCATATATTCACTTCCAGATCCATTGGTAAACTACAGGGCCTACAAACTTTGAA | 1674 CATGCCGAGCACATACATTGCAGCACTACCAAGTGAGATCAGTAAACTCCAATGTCTGCA :           | 1734 TACTCTTCGTTGTAGTAGAAAGTTTGTTTCTGACAACTTTAGTCTAAACCACCAATGAA :    | 1794 GTGCATAACTAACACAATATGCCTGCCTAAAGTATTCACACCTTTAGTTAG                | 1854 TCGTGCAATACAAATTGCTGAATTGCACATGGCCACCAAAAGTTGCTGGTATAAATCATT | 1914 CGGTGTGAAGGTACCCAAAGGAATAGGTAAGTTGCGAGACTTACAGGTTCTAGAGTATGT :      | 1974 AGATATCAGGGGACCAGTAGTAGAGCAATCAAAGAGCTGGGGCAGTTAAGCAAGC                                    | 2034 GAAATTAGGTGTGATGACAAATGGCTCGACAAAGGAAAAATGTAAGATACTTTGTGCAGC ;<br>                                                                                               | 2094 CATTGAGAAGCTCTTCCCTCCAATATCTCTATGTGAATGCTGCAGGAATCTCAGATGG ;                                  | 2154 TGGAACACTTGAGTGCCTAGATTCTATTTCCTCTCCTCCTCCCCTACTGAGGACACTCGT 2 | 2214 GTTGTATGGAAGTCTTGAAGAGGCCTAACTGGATTGAGCAGCTCACCTCACCTGAAGAA 2<br>                                                                                                                                               | 2274 GAICTACTTATTGAGGAGCAAACTAAAGGAAGGTAAAACCATGCTGATACTTGGGGCATT 2<br>                                                                                       | 2334 GCCCAACCTCATGGTCCTTGATCTTTATCGGAAAGCTTACCTTGGGGAGAAGCTAGTT 2<br> | 2394 CAAAACAGGAGCATTCCCAAATCTTAGAACACTTTCGATTTACGATTTGGATCAGCTAAG 2<br> | 2454 AGAGATTAGATTTGAGGACGGCAGCTCGCCCCAGTTGGAAAAGATAGAAATCAGATTCTG 2<br> | 2514 CAGGTIGGAATCAGGGATTATTGGTATTATCCACCTTCCAAGGCTCAAGGAGATTTCACT 2<br> | 2574 TGGATACGAAAGTGGCTGGCCTTGCTCAGCTGGAGGGAGAGAGTGCGCACACCC 2 | 2634 AAATCACCCCGTGCTGCGAAAGAGGGACCGAAGTGATCACGACCTTGCTTG |
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| S G                                                                           | & B                                                                                                                                                                                             | <b>&amp;</b> 8                                                                | 8 8                                                                   | <b>상</b> 됨                                                              | & a                                                               | \$ A                                                                     | <b>&amp;</b> 8                                                                                  | & 8                                                                                                                                                                   | ъ д                                                                                                | & a                                                                 | è a                                                                                                                                                                                                                  | & 4g                                                                                                                                                          | o da                                                                  | පි පි                                                                   | \$ 6<br>6                                                               | & 9g                                                                    | 8 8                                                           | ò                                                        |
| OY 2409 CCCAAATCTTAGAACACTTTCGATTTACGATTTGGATCAGCTAAGAGAGATTAGATTTGA 2468<br> | OY 2469 GGACGCGCGCCCCAGTTGGAAAAGATAGAAATCTGCAGGTTGGAATCAGG 2528                                                                                                                                 | OY 2529 GAITATIGGTATTAICCACCTTCCAAGGCTCAAGGAGATTTCACTIGGATACGAAAGTAA 2588<br> | OY 2589 AGIGGCIGGGCTTGCTCAGCTGGGGAAGAGTGCGCACACCCAAATCACCCCGTGCT 2648 | OY 2649 GCGAAAGAGGAGGACCAAGTGATCACGACCTTGCTTGTGACGCGGAAGGATCCCCTGT 2708 | OY 2709 TGAAGTGGAAGGATCCCTCCCGAAGGA 2741                          | RESULT 12<br>US-10-656-394A-15<br>: Seminore 15 Application IS/106662948 | Publication No. US20040210957A1 GENERAL INFORMATION: APPLICANT: Wang et al. TITE. OF INVENTION: | ; TITLE OF INVENTION: broad-spectrum resistance gene Fi2; FILE REFERENCE: 035718/252062; CURRENT APPLICATION WINGBER: US/10/656,394A; CHEBENT STILMS DATE: 2003-00-00 | NUMBER OF SECOND NOS: 16 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 15 ; TANCET. 24.2 |                                                                     | <pre>// MAND/AZI: MISC_Leadle. // LOCATION: 2014, 2043, 2099, 2114, 2154, 2172, 2178, 2199, 2205, 2226, // LOCATION: 2268, 2299, 2333, 2337, 2339, 2356 // OTHER INFORMATION: n = A,T,C or G US-10-656-394A-15</pre> | Query Match 45.2%; Score 1354.2; DB 18; Length 2422; Best Local Similarity 94.1%; Pred. No. 0; Matches 1407; Conservative 0; Mismatches 88; Indels 0; Gabs 0: | CGAATTCATGATALCATCCGTGATATCACAGTTTCAATCTC 13                          | 4-4                                                                     |                                                                         | TATTCGATCATTAGCTATTTTTGGTGACAGACCCAAGAGTCTAGCACATGCAGTTTGTCC            | AGATCAATTGAGGATGTTACGGGTCTTGGATCTTGAAGATGTGACATTCTTAATCACTCA  | 241 AGAICAAITGAGGAIGITACGGGICTTGGAICTTGAAGATGTGACATTC    |

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| 215   CCCACACCTACTACTACTACTACTACTACTACACACACA | GGTAAACTACAGGCCTACAAACTTTGAACATGCCGAGCACTACATGCAGGCTAACCA GGTAAACTACAGGCCTACAAACTTTGAACATGCCGAGCACTACCA                                                                                   |
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|                                               | Db 730 GGTGCTGATTCATTAGACAAACTCTTGAAGAGAATTTAGTGGAAGTCTGTGCTGTGCAAGTC 789  Oy 565 CATCATCTTTCTGAGTACCTGAAGAGACAAGAGAGAAGAGTCTTGTTCTTA 624  Db 790 CAGCATCTCGCTGTTTGAAGAGCTTGAAGAGAAAAGAAA |

Length 2925;

DB 18;

us-10-656-394a-11.rnpb

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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21 (53221) CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 SEQ ID NOS: 204966 SEQ ID NOS: 204966 LENGTH: 2925
                                                                                             PEATURE:
OTHER INFORMATION: Clone ID: PAT MRT4530_44401C.1
                                                                              TYPE: DNA
ORGANISM: Oryza sativa
                                                                                                          ; OTHER INFORMATIC
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Sequence 41016, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Li, Ping

RESULT 14 US-10-437-963-41016

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Publication No. US20040210957A1

GENERAL INFORMATION:

APPLICANT: Wang et al.

TITLE OF INVENTION:

FILE REPRENCE: 035718/522062

FILE REPRENCE: 035718/522062

CURRENT APPLICATION UNMER: US/10/656,394A

CURRENT PILING DATE: 2003-09-05

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSEQ for Windows Version 4.0

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LENGTH: 2982
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| Claim 1; SEQ ID NO 12; 120pp; English. The invention relates to novel broad-spectrum resistance gene Pi2 and th                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| Claim 1; SEQ ID NO 12; 120pp; Engli The invention relates to novel broa NBS(1-6) genes present in the Pi2 g disease resistance nucleic acid mol                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| Claim 1; SEQ ID NO 12; 120pp; English.  The invention relates to novel broad-spectrum resistance gene Pi2 and the NSS(1-6) genes present in the Pi2 gene Cluster region. The rice Pi2-like                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| Claim 1; SEQ ID NO 12; 120pp; English. The invention relates to novel broad-spectrum resistance gene Pi2 and th NBS(1-6) genes present in the Pi2 gene cluster region. The rice Pi2-like                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| Claim 1; SEQ ID NO 12; 120pp; English.  The invention relates to novel broad-spectrum resistance gene Pi2 and the NBC 11-51 research in the Di2 and chiefer resist me the Di2 like                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| Claim 1; SEQ ID NO 12; 120pp; English. The invention relates to novel broad-spectrum resistance gene Pi2 and th                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| Claim 1; SEQ ID NO 12; 120pp; English.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| Claim 1; SEQ ID NO 12; 120pp; Engli                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
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| disease resistance in plants, useful for creating or enhancing disea                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
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| 05-SED-2003, 2003C3-043-04                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| 18-MAR-2003: 2003US-0455713P                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| 09-SEP-2002; 2002US-0409216P                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
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                                                                                             GLGKTALSRKIFESEEDIRKNFPCNAWITVSQSFHRIELLKDMIRQLLGPSSLDQLLQEL 180
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                                                             GNOSCLAIDSYAEDIRNOSARNVDEAELVGFSDSKKRLLEMIDTNANDGPAKVICVVGMG
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ADM72245 standard; protein; 1032

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                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to novel broad-spectrum resistance gene Pi2 and the NBS(1-6) genes present in the Pi2 gene cluster region. The rice Pi2-like disease resistance nucleic acid molecules are useful for enhancing disease resistance in plants. The present sequence represents a rice NBS4
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for creating or enhancing disease
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                                                                            gene therapy; rice; disease resistance
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82.5%; Score 4237; D

Best Local Similarity 84.2%; Pred. No. 0;

Matches 854; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                     disease resistance disease resistance disease resistance in plants, useful resistance in plants.
                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 8; 120pp; English.
                                                                                                                                                                                             09-SEP-2002; 2002US-0409216P.
18-MAR-2003; 2003US-0455713P.
05-SEP-2003; 2003US-00656394.
                                                                               protectant;
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                                                       O. minuta NBS4 polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptide.
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          ADM72245;
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           Nucleic acids enc
and NBS3, useful
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plant.
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transgenic plant;
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01-FEB-2002; 2002US-0353304P.
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N-PSDB; ADI57171.
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S) proteins NBS1, NBS2
Magnaporthe grisea
                                                                                                                                    The invention comprises the amino acid and coding sequences of nucleotic binding site (NBS) proteins from the Oryza minuta Pi9 locus (bacterial blight and rice blast resistance genes). The DNA sequences may be used markers for resistance to infection with Magnaporthe grises in plant breeding programs. The present amino acid sequence represents an NBS protein encoded by a gene from the Oryza minuta Pi9 locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |: | :: | | :: | | EVSSRNTRYNLVEPISSGTED--DMDSYAEDIRNQSARNVDBAELVGFSDSKKRLLEMID
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MDSDRRDHDLGAEAEGSSIEVQTADPVPDAEGSVTVAVEATDPLPEQEGESSQ 1071
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                                                                                                                                                            958
                                                                                                                         DGSSPQLEKIEIRFCRLESGIIGIIHLPRLKEISLGYESKVAGLAQLEGEVRTHPNHPVL 883
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SKLKEGKTWLILGALDNIMVLYLYWNAYLGEKLVPKTGAFDNLRTLRIYELDQLREMRFE
                                                                                                                                               DGSSPLLEKIEISCCRLESGIIGIIHLPRLKEISLEYKSKVARLGQLEGEVNTHPNRPVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  binding site; NBS; Pi9 gene; bacterial blight; rice blast; ding; transgenic plant; plant.
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79.0%; Pred. No. 0;
ive 21; Mismatches
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01-FEB-2002; 2002US-0353304P.
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Best Local Similarity 79.0
Matches 848; Conservative
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N-PSDB; ADI57175
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plant breeding;
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   TLGYNHLPSHLKPCFLYLSIFPEDFEIQRNRLVGRWIAEGFVRPKVGMTTKDVGESYFNE
                                LINRSMIQRSRVGIAGKIKTCRIHDIIRDITVSISRQENFVLLPMGDGSDLVQENTRHIA
                                               LINRSMIQRSRVGTAGKIKTCRIHDIIRDITVSISRQENFVLLPMGDGSDLVQENTRHIA
                                                                                        FHGSMSCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLBDVTFLITQKDFDR
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N-PSDB; ADI57167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KNMQKMVERIVNKCGRLPLAILTIGAVLATKQVSEWEKFYEQLPSELEINPSLEALRRMV 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to novel broad-spectrum resistance gene Pi2 and the NBS(1-6) genes present in the Pi2 gene cluster region. The rice Pi2-like disease resistance nucleic acid molecules are useful for enhancing disease resistance in plants. The present sequence represents a rice NBS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---GRSNGGPVVGMVASGNQSCLAIDSYAEDIRNQSARNVDEAELVGFSDSKKRLLEMID 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |: | | : | | : | | EVSSRNTRYNLVEPISSGTED--DMDSYAEDIRNQSARNVDEAELVGFSDSKKRLLEMID 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AFPKNNKKGSRIVITTRNVDLAEKCATASLVYHLDFLQMNDAISLLLRKTNKNHEDMESN 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 KDELLKVWAEQIRDLSYDIEDSLDEFKVHIESQTLFRQLVKLRERHRIAIRIHNLKSRVE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNANDGPAKVICVVGMGGLGKTALSRKIFESEEDIRKNFPCNAWITVSQSFHRIELLKDM 163
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                                                                                                                                                                                                                                                                                                                                                           New rice Pi2-like disease resistance nucleic acid molecule that confers disease resistance in plants, useful for creating or enhancing disease resistance in plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLGYNHLPSHLKPCFLYLSIFPEDFEIKRNRLVGRWIAEGFVRPKVGMTTKDVGESYFNE
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                                                             resistance
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                                                            disease
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                                                          Pi2; NBS2; plant protectant; gene therapy; rice;
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Best Local Similarity 82.5%; Pred. No. 0;
Matches 837; Conservative 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 4; 120pp; English
                                                                                                                                                                                                        09-SEP-2002; 2002US-0409216P.
18-MAR-2003; 2003US-0455713P.
05-SEP-2003; 2003US-00656394.
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                             minuta NBS2 polypeptide
(first entry)
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                                                                                      Oryza minuta.
03-JUN-2004
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DDLLKVWAEQVRDLSYNIEDCLDEFKVHVESQSLAKQLMKLGERHRIAVQIRNLKSRIEE 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RFEDGSSPQLEKIEIRFCRLESGIIGIIHLPRLKEISLGYESKVAGLAQLEGEVRTHPNH
                                                            VASGNOSCLAI ------DSYAEDIRNOSARNVDEAELVGFSDSKKRLLEMIDTN
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LLRSKLKEGKTMLILGALPNLMVLDLYRKAYLGBKLVFKTGAFPNLRTLSIYDLDQLREI
             Pi2; NBS1; plant protectant; gene therapy; rice; disease resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New rice Pi2-like disease resistance nucleic acid molecule that disease resistance in plants, useful for creating or enhancing dresistance in plants.
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55.1%; Pred. No. 2.4e-236;
ive 129; Mismatches 229;
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2003US-00656394.
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N-PSDB; ADM72238
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05-SEP-2003;
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                                              The invention comprises the amino acid and coding sequences of nucleoti binding site (NBS) proteins from the Oryza minuta Pi9 locus (bacterial blight and rice blast resistance genes). The DNA sequences may be used markers for resistance to infection with Magnaporthe grises in plant breeding programs. The present amino acid sequence represents an NBS protein encoded by a gene from the Oryza minuta Pi9 locus.
                                                                                                                                                                                                                                                                                                                                                                     IAFHGSMSCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLEDVTFLITQKDF
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            TNDGPAKVICVVGMGGLGKTTLARKAYENKEHM-KNFSCCAWITVSQSFDRKEILKQMIR
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plant breeding; transgenic plant; plant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QDELVKVWAEQVRDLAYDIEDCLQEFAVHVGHÓSLSMOLIKLCHRHRIAVQIRNLKQRVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 42.3%; Score 2170.5; DB 8; Best Local Similarity 49.1%; Pred. No. 2.4e-194; Matches 478; Conservative 155; Mismatches 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 87; 136pp; English
                                           27-JAN-2003; 2003US-00352179
                                                                                       25-JAN-2002; 2002US-0352106P
01-FEB-2002; 2002US-0353304P
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N-PSDB; ADI57169.
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ANDGPAKVICVVGMGGLGKTALSRKIFESEEDIRKNFPCNAWITVSQSFHRIELLKDMIR 165
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                                                                                                                                                                                                                                                                                                                                                                                                VASGN------QSCLAIDS---YAEDIRNQSARNVDEAELVGFSDSKKRLLEMIDTN 105
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                                                                                                                                                                                                                                                                                                                                                       SILLKVWVQQVRDLSYDIEDCLDEFTVHVGSQNLSRQLMKLKDRHRIAIQIRNLRTRIEE
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markers for resistance to infection with Magnaporthe grisea in plant breeding programs. The present amino acid sequence represents an NBS protein encoded by a gene from the Oryza minuta Pi9 locus.
                                                                                                                                   Length 1054;
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                                                                                                                              / Match 40.9%; Score 2103.5; DB 8; Length Local Similarity 45.9%; Pred. No. 5.4e-188; Nes 480; Conservative 131; Mismatches 244; Indels
                                                                                                                                                                                                                                                                                                               -----FRHGVGRSNGG-----
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  DISKCSNIGMDWSHVRSLTLFGNERPKGLSPSFCFPQLKMLRVLDLQDVKFGMTQKDIGK 594
                                                                                                                                                         RKFVSDNFSLNHPMKCITNTICLPKVFTPLVSRDDRAIQIAELHMATKSCWYK---SFGV 640
                                                                                                                                                                                                                                               KVPKGIGKLRDLQVLEYVDIRRTSSRAIKELGQLSKLRKLGVMTNGSTKEKCKILCAAIE 700
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                                                                                            Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2 and NBS3, useful for producing plants resistant to Magnaporthe grisea infection.
                                                                                                                                                                                  GRPNSGDFNLNDPKDCLIAFSCLPLLMAATDS-DERNKIIAELHVGCSSQWSPNGGTYGV
                                                                      IALLCHLKYLSIGYSSSIYSLPRSIGKLQGLQTLNMPSTYIAALPSEISKLQCLHTLRCS
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Novel polypeptide and DNA encoding it used to produce plants resistant to fungal blast disease.
                                                                                                                                                                                             347 YNHLPSHLKPCFLYLSIFPEDFEIKRNRLVGRWIAEGFVRPKVGMTTKDVGESYFNELIN 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention provides a protein which confers resistance to blast disease onto plants. The blast disease-resistance (Pi-b) protein can be expressed by standard recombinant methodology. The novel Pi-b gene is used to produce transgenic plants resistant to the rice blast disease, which will control the disease and increase crop yields. The present sequence represents the rice Pi-b protein. The resistance gene Pi-b is located at the end of the long arm of rice chromosome 2 and displays
181 KDGPTKVVCVVGMGGLGKTTIARKIYESKEDIAKNFSCCAWITVSQSFVRVELLKDLMVK
                                                                                                 SDIITKIVKKCGYLPLAILTIGGVLSTKEIREWETFYSQIPSELESNPNLEAMRRIVTLS
                                                                                                                                                                                                                                                                     SRYCSETSLDWSIIRSLTWFGERSVELEHSVCSSQLRMLRVLDLIDAQFSITQNDVDNIV
                                          KNNKKGSQIVITTWNVDLAEKCATASLVYHLDFLQMNDAITLLLRKTNKNHEDMESNKNM
                                                                                                                                       QKMVERIVNKCGRLPLAILTIGAVLATKQVSEWEKFYEHLPSELEINPSLEALRRMVTLG
                                                                                                                                                                                                                                                                                                            SMSC-KTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLEDVTFLITQKDFDRIA
                           LLGPSSLDQLLQELQGKVVVQVHHLSEYLIEELKEKRYFVVLDDLWILHDWNWINEIAFP
                                                                                                                                                                                                                                                      RSMIQRSRVGIAGKIKTCRIHDIIRDITVSISRQENFVLLPMGDGSDLVQENTRHIAFHG
                                                                                                                                                                                                                                                                                                                                                                  LICHLKYLSIG----YSSSIYSLPRSIGKLQGLQTLNMPSTYIAALPSEIS 572
                                                                                                                                                                                                                                                                                                                                                                               Yamanouchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blast disease; rice; Pi-b gene; blast disease-resistance gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NORQ ) NAT INST AGROBIOLOGICAL RESOURCES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY49434 standard; protein; 1205
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N-PSDB; AAZ46679, AAZ46680.
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Ishimaru
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    895 NIQGLESGIVGIIHLPRLKEISLGYGSKVARLGQLEGEVRTHPNHPVLRMREDRSDHDLA 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 SILLKVWVQQVRDLSYDIEDCLDEFTVHVGSQNLSRQLMKLKDRHRIAIQİRNLRTRIEE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----DSYAEDIRNQSARNVDEAELVGFSDSKKRLLEMIDTNA 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MADTVLSIAKSLVGSAVSKVASVAADKMIMLLGVQKEIWFIKDELQTIQAFLIAAEASKK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New rice Pi2-like disease resistance nucleic acid molecule that conferm
disease resistance in plants, useful for creating or enhancing disease
resistance in plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----FRHGVGRSNGGPVVGMVASGNQSCLAI
              ----LESGIIGIIHLPRLKEISLGYESKVAGLAQLEGEVRTHPNHPVLRKREDRSDHDLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.0%; Score 1748; DB 8; Length 6 54.2%; Pred. No. 8.1e-155; ive 86; Mismatches 132; Indels
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                                                                                    CDAEGSPVEVEATOPLPEQEGESSOR 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; SEQ ID NO 6; 120pp; English.
                                                                                                                                                                   660 AA
                                                                                                                                                                                                                                                                                                                                                                                                                        09-SEP-2002; 2002US-0409216P.
18-MAR-2003; 2003US-0455713P.
05-SEP-2003; 2003US-00656394.
                                                                                                                                                                                                                                                                                                                                                                                              08-SEP-2003; 2003WO-US027913.
                                                                                                                                                                  ADM72243 standard; protein;
                                                                                                                                                                                                                                                      O. minuta NBS3 polypeptide
                                                                                                                                                                                                                          (first entry)
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Best Local Similarity 54.2
Matches 353; Conservative
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                                                                                                                                                                                                                                                                                                              Oryza minuta.
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                                                                                                                                                                                               ADM72243;
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The invention relates to novel broad-spectrum resistance gene Pi2 and the NBS(1-6) genes present in the Pi2 gene cluster region. The rice Pi2-like disease resistance nucleic acid molecules are useful for enhancing disease resistance in plants. The present sequence represents an O. minuta Pi2 gene predicted amino acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KNHEDMESNKNMQKMVERIVNKCGRLPLAILTIGAVLAT -- KQVSEWEKFYEHLPSELEI 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRIIVSSTQVEVASLCAGQESQASELKQLSADQTLYAFYDKGSQIIEDSVKPVSISDVAI 311
                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid molecule that confers
for creating or enhancing disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 MIRQL-LGPSSLDQLLQ----ELQGKVVVQVHHLSEYLIEELKEKRYFVVLDDLWILHDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VASGNQSCL-----AIDSYAEDIRNQSARNV-----DEAELVGFSDSKKRLLEMI
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                                                                                                                                                                     Pi2; NBS1; plant protectant; gene therapy; rice; disease resistance.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1205;
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llarity 31.4%; Pred. No. 5.6e-87;
Conservative 184; Mismatches 354;
                                                                                                                                              amino acid sequence
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| KGGELKRKIREQLARNPNQPII 1204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 5; 120pp; English
                                                                       protein; 1205
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18-MAR-2003; 2003US-0455713P.
05-SEP-2003; 2003US-00656394.
                                                                                                                                               O. minuta Pi2 gene predicted
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------HKALARRDAWTFACCVKFPSIMTGVHEBEGAMVPSGIRKLKDLHTLRNIN 950
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                                                                                                                                                                                             DINANDGPAKVICVVGMGGLGKTALSRKIFESEEDIRKNFPCNAWITVSQSFHRIELLKD 162
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                                                                         Gaps
                                               Query Match 20.1%; Score 1033; DB 3; Length 1205; Best Local Similarity 31.4%; Pred. No. 5.6e-87; Matches 308; Conservative 184; Mismatches 354; Indels 136;
                                                                                                ARSLVGSAISKAASAADETSLL----LGVEKDIWYLFRHG--VGRSNGGPV-
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resistance to blast
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                                                                                                                                                                                                                                                                                                           The invention relates to the isolation of novel rice blast fungus (Pyricularia grisea; also known as Magnaporthe grisea) resistance genes (Incom rice strain BL-1. The genes are designated Pi-b (AAA11349) and Pi-b' (AAA11351). The genes can be used for creating rice which has high blast fungus resistance. This sequence represents the protein encoded by the Pi gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDGSDLVQENTRHIA----FHGSMSCKTGL-DWSIIRSLAIFGDRPKSLAHAVCPDQLRM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :: | : : | :: | : : | : : | : : | : : | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIRQL-LGPSSLDQLLQ----ELQGKVVVQVHHLSEYLIEELKEKRYFVVLDDLWILHDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAEQLHKGSSKKEELLENRVSSKKSLASMEDTELTGQLKRLLEKKSCLIVLDDFSDTSEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRVLDLEDVTPLITQKDFDRIALLCHLKYLSIGYSSSIYSLPRSIGKLQGLQTLNMPSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IAALPSEISKLOCLHTLRCSRK--FV-SDNFSLNHPMK---CITNTICLP---KVFTPLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VKALPKTIIKLOKLOYIHAGRKTDYVWEBKHSLMORCRKVGCICATCCLPLLCEMYGPL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --YKSFGVKVPKGIGKLRDLOVLEYVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IRRISSRAIKELGQLSKLRKLGVMTNGSTKEKCKILCAAIEKLSSLQYLYVNAAGISDGG
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                                                                                             rice
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARSLVGSAISKAASAAADETSLL-----LGVEKDIWYLFRHG--VGRSNGGPV-
                                                                                        for creating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.1%; Score 1033; DB 3; 1
ilarity 31.4%; Pred. No. 6e-87;
Conservative 184; Mismatches 354;
                                                                                             genes, useful
                                                                                                                                                                                                                           Claim 26; Page 20-23; 36pp; Japanese.
                                                                                             related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SRDDRAIQIAELHMATKSCW--
                                                                               A blast-resistant gene and religrade of high blast resistance.
N-PSDB; AAA11349, AAA11350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 308; Conserv
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                                                                                                                                                                                                                                                                                  241 LFGEEVLKKRLRELEGK-VPQVDDLASYLRTELNERRYFVVLDDVWSTDSWKWINSIAFP 299
                                                                                                                                                                                                                                                                                                                                                                       347 YNHLPSHLKPCFLYLSIFPEDFEIKRNRLVGRWIAEGFVRPKVGMTTKDVGESYFNELIN 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        407 RSMIQRSRVGIAGKIKTCRIHDIIRDITVSISRQENFVLLPMGDGSDLVQENTRHIAFHG 466
                                                                                                                                                                       107 NDGPAKVICVVGMGGLGKTALSRKIFESEEDIRKNFPCNAWITVSQSFHRIELLKDMIRQ 166
                                                                                                                                                                                                                                                         LLGPSSLDQLLQELQGKVVVQVHHLSEYLIBELKEKRYFVVLDDLWILHDWNWINBIAFP 226
                                                                                                                                                                                                                                                                                                                                              KNNKKGSQIVITTWNVDLAEKCATASLVYHLDFLQMNDAITLLLRKTNKNHEDMESNKNM 286
                                                                                                                                                                                                                                                                                                                                                                                                                                 287 QKMVERIVNKCGRLPLAILTIGAVLATKQVSEWEKFYEHLPSELEINPSLEALRRMVTLG 346
                                        61 SILLKVWVQQVRDLSYDIEDCLDEFTVHVGSQTLSRQLMKLKDRHRIAVQIRNLRTRIEE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid molecule encoding a resistance gene homolog, useful for
producing disease resistant transgenic plant.
57
--FRHGVGRSNGGPVVGM
                                                                                  VASGNOSCLAIDS-----YAEDIRNOSARNVDEAELVGFSDSKRLLLEMIDTNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene homologue; RGH; transgenic plant; crop protection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sorghum resistance gene homologue S6-1-encoded protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            360 SDIITKIVKKCGYLPLAILTIGGVLATK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1(b); Page 88-90; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-182422/16.
N-PSDB; AAZ58293, AAZ58294, AAZ58295.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0093290P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-JUL-1998;
15-JUL-1999;
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                                                                                                                                     The invention comprises the amino acid and coding sequences of nucleotide binding site (NBS) proteins from the Oryza minuta P19 locus (bacterial blight and rice blast resistance genes). The DNA sequences may be used as markers for resistance to infection with Magnaporthe grisea in plant breeding programs. The present amino acid sequence represents an NBS protein encoded by a gene from the Oryza minuta P19 locus.
                                                                                                             PNLMVLDLYRKAYLGEKLVFK---TG-AFPNLRTLSIYDLDQLREIRFEDGSSPQLEKIE 834
                                                                                                                                                                                             -----GYESKVAGLAQ 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2 and NBS3, useful for producing plants resistant to Magnaporthe grisea infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleotide binding site; NBS; Pi9 gene; bacterial blight; rice blast; plant breeding; transgenic plant; plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza minuta Pi9 locus nucleotide binding site (NBS) protein #6.
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The present sequence is that of the predicted full-length protein encoded by the novel sorghum resistance gene homologue (RGH) S6-1. The invention provides 13 novel maize, sorghum and rice RGH gene families (see AAZS8273-95) and their protein products (see AAYS8842-54). The novel RGH sequences can be used for the production of transgenic plants (and their cells, tissues and seeds) having improved resistance to disease. Expression of a novel RGH gene confers disease resistance to a plant pinteracting with the complementing phytopathogen avirulence gene product the invention find use in controlling plant pathogen. The methods of pathogens, viruses, nematodes and insects
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Sequence 953 AA

41; Gaps 16.7%; Score 857; DB 3; Length 953; llarity 27.8%; Pred. No. 1.5e-70; Conservative 170; Mismatches 340; Indels 236; Query Match Best Local Similarity Matches 287; Conserva

| Db 233PDIKKILRHILCQYSCRECGNNEIWDEQQLINTTRQFLKDKRYFIVIDDIWSIS 286        | 41<br>61<br>117<br>117<br>177<br>155<br>232<br>215<br>286 | 3 ETVLSMARSLVGSAISKAASAAADETSLLLGVEKDIWYL                          | 2 2 42 42 42 42 42 42 42 42 42 42 42 42 |
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|                                                                         | 273                                                       | 216 DWNWINEIAFPKNNKKGSQIVITTWNVDLAEKCATASLVYHLDFLQMNDAITLLLRKT 273 | 216                                     |
|                                                                         | 215                                                       | RIELLKDMIRQLLGPSSLDQLLQELQGKVVVQVHHLSEYLIEELKEKRYFVVLDDLWILH 2     | 156                                     |
| QY 156 RIELLKDMIRQLLGPSSLDQLLQELQGKVVVQVHHLSEYLIEELKEKRYFVVLDDLWILH 215 | 232                                                       | KLIKLITEREGITTQLSVVSIVGFGGLGKTTLANEVYQKLEGQFDYRAFVSVSQK 2          | 178                                     |
| н п                                                                     | 155                                                       | RLLEMI-DINANDGPAKVICVVGMGGLGKTALSRKIFESEEDIRKNFPCNAWITVSQSFH       | 97                                      |
|                                                                         | 177                                                       | HWIAKKIQRLKCHVIEASNRRGRYRVDDAVPRLSRTSIDPRLPALYTETTRLVGVDGPRD 1     | 118                                     |
| 4 1 1                                                                   | 96                                                        |                                                                    | 74                                      |
| 4 4 4                                                                   | 117                                                       | EQSKCWMKEVRELSYDIEDSIDSFIFSLGCESNSEPRGFKGFVGRCLNLFADAKTR 1         | 62                                      |
|                                                                         | 73                                                        |                                                                    | 42                                      |
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SD--LVQENTRHIA--FHG--SMSCKTGLDWSIIRSLAIFG--DRPKSLAHAVCPDQLRM 503

IAALPSEI---SKLOCLHTLRCSRKFVSDNFSLNHPMKCITNTICLPKVFTPLVSRDDRA 620

634 IKRLPQSVVLLRRLTCL---------LVNSL------

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## ALIGNMENTS

| RESULT 1 A57072 disease resistance prot C;Species: Arabidopsis C;Date: 03-0ct-1995 #se C;Accession: A57072 R;Grant, M.R.; Godiard, Science 269, 843-846, 1 A;Title: Structure of t A;Recence number: A57 A;Accession: A57072 A;Status: preliminary; A;Nolecule type: DNA A;Residues: 1-926 GRA> A;Cross-references: UNI C;Generics: A;Gene: RPMI C;Superfamily: disease F;S22-664/Domain: leuci; F;628-650/Domain: leucii | RESULT 1 A57072 A650072 A650072 A650072 A650072 A650072 A66ease resistance protein RPM1 - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004 C;Accession: A57072 R;Grant, M.R.; Godiard, L.; Straube, E.; Ashfield, T.; Lewald, J.; Sattler, A.; Innes, R Science 269, 843-846, 1995 A;Title: Structure of the Arabidopsis RPM1 gene enabling dual specificity disease resist A;Title: Structure of the Arabidopsis RPM1 gene enabling dual specificity disease resist A;Title: Structure of the Arabidopsis RPM1 gene enabling dual specificity disease resist A;Title: Structure of the Arabidopsis RPM1 gene enabling dual specificity disease resist A;Title: Structure of the Arabidopsis RPM1: Title: Britle: A;Title: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: Britle: B |
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| Query Match<br>Best Local<br>Matches 28                                                                                                                                                                                                                                                                                                                                                                                   | <pre>Query Match Best Local Similarity 28.2%; Pred. No. 1.5e-46; Matches 283; Conservative 174; Mismatches 343; Indels 202; Gaps 36;</pre>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| Qy 8                                                                                                                                                                                                                                                                                                                                                                                                                      | 8 MARSLVGSAISKAASAAADETSLLLGVEKDIWYLFRHGVGRSNGGP 53<br>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| Qy 54<br>Db 58                                                                                                                                                                                                                                                                                                                                                                                                            | 54 VVGMVASGNQSCLAIDSYAEDIRNQSARNVDEAE 87                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| Oy 88<br>Db 117                                                                                                                                                                                                                                                                                                                                                                                                           | J.VGFSDSKKRLLEMIDTNANDGPAK                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| Qy 113<br>Db 173                                                                                                                                                                                                                                                                                                                                                                                                          | VICVVGMGGLGKTALSRKIFESEEDIRKNFPCNAMITV 150<br>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| Qy 151<br>Db 232                                                                                                                                                                                                                                                                                                                                                                                                          | . SQSFHRIELLKDMIRQLLGPSSLDQLLQELQGKVVVQVHHLSEYLIEELKEKRYF 205<br>   -                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| Qy 206<br>Db 283                                                                                                                                                                                                                                                                                                                                                                                                          | VVLDDLWILHDWNWINEIAFPKNNKKGSQIVITTWNVDLAB-KCATASLVYHLDFLOWND 264<br>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |

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probable disease resistance protein F23H11.10 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLLPMGDGSDLVQEN---TRHIAFH--GSMSCKTGLDWSIIRSLAIFGD-----RPKSLA 493
                                                                                                                                                                                                                              LHDWNWINEIAFPKNNKKGSQIVITTWNVDLAEKCATASLVYHLDFLQMNDAITLLLKKT 273
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                                                                                                                                                                                                                                                                                                                             SSRRDKTEF-KVDEAMGKEMVTYCGGLPLAVKVLGGLLAKKHTVLEWKRVHSNIVTHIVG
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                                                                                                                                                                         NPSL-----BALRRMVTLGYNHLPSHLKPCFLYLSIFPEDFEIKRNRLVGRWIAEGFVRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LYRKAYLGEKLVFKTGAFPNLRTLSIYDLDQLREIRFEDGSSPQLEKIEIRFCRLESGII
                                                                                                --ELVDHLVENDSVQVVSVSGMGGIGKTTLARQVFH-HDIVRRHFDGFSWVCVSQQFTR-
                                                                                                                                                                                                                                                                                                         NKNHEDMESNKNMOKMVERIVNKCGRLPLAILTIGAVLATKQ-VSEWEKFYEHLPSELEI
GVGRSNGGPVVGM------VASGNQSCLAIDSYAEDIRNQSARNVDBAELVGFSDSKKR
                             GITKRISEVIVGMOSLGIQHIADGGGRSLSLQERQREIRQTFSRN-SESDLVGLDQSVE-
                                                                          LLEMIDTNANDGPAKVICVVGMGGLGKTALSRKIFBSEEDIRKNFPCNAWITVSQSFHRI
                                                                                                                                                   ELLKDMIRQLLGPSSLDQLLQEL----QGKVVVQVHHLSEYLIBELKEKRYFVVLDDLWI
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|LCLNLGVADRLLVHVPNVLKEMQELRYLRLPRSM------PAK---
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: F96573
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, W.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunder, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Verter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Rcession: F96573
A;Status: preliminary
A;Accession: F96573
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C;Genetics:
A;Gene: F12M16.25
A;Map position: 1
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                                                                                                                                                                                                                  CDVYNDDSDGDDAAETMENYGSRHLCIQKEMT-PDSIRATNLHSLLVCSSAKHKM--ELL 577
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                                                                                                                                                                                             --VLLPMGDGSDLVQ--EN--TRHIAFHGSMSCKTGLDWSIIRSLAIFGDRPKSLAHAVC 497
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   AWVLFSNKAFPASLEOCRTONLEPIARKLVERCOGLPLAIASLGSMMSTKKFESEWKKVY 400
                                         EHLPSELEINPSLEALRRMVTLGYNHLPSHLKPCFLYLSIFPEDFEIKRNRLVGRWIAEG
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probable disease resistance protein F9K23.8 [imported] - Arabidopsis thaliana probable disease resistance protein F9K23.8 [imported] - Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: O:Z-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: F96617
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Cressy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.; Gonway, A.B.; Conway, A.R.; Cressy, T.H.; Dewar, K.; A;Athores: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.W.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Praser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
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                                                                 821 RFEDGSSPOLEKIEIRFCRLESGIIGIIHLPRLKEISLGYESKVAGLAOLEGEVRTHPNH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 322 FYEHLPSEL--EINPSLEALRRMVTLGYNHLPSHLKPCFLYLSIFPEDFEIKRNRLVGRW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         437 ISRQENFVLLPMGDGSDLVQENTRHIAFHGSMSCKTGLDWSIIRSLAIFGDRPKSL--AH
                               LLRSKLKEGKTMLILGALPNLMVLDLYRKAYLGEKLVFKTGAFPNLRTLSIYDLDQLREI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 907;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.1%; Score 675.5; DB 2; 28.1%; Pred. No. 3.9e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       al Similarity 28.1%; Pred. No. 3.9e-35; 223; Conservative 149; Mismatches 313;
                                                                                                                                                                                                                                 IVEEGSMPLLHTLHIVDCK-
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                                                                                                                                                                                                                                                                                                      PVLRKREDRSDHD 893
                                                                                                                                                                                                                                                                                                                                                    KVFQKKVSKGGED 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Residues: 1-907 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Status: preliminary
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          Chin, C.W.; Chung, M.E.; Palm, C.J.; Federapiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Albere, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Khaykin, E.; Kim, C.C., J., J., J., H.; Y.; Roney, T.; Roney, T.; Roher, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Hele: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Residus: preliminary
A;Residus: Lego, S.L.; A;Residus: Lego, S.C.; Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conton Conto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 IDSYAEDIRNQSARNV----DEAELVGFSDSKKRLL-EMIDTNANDGPAKVICVVGMGGL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKTALSRKIFESEEDIRKNFPCNAWITVSQSFHRIELLKOMIRQLLG---PSSLDQLLQE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GRLPLAILTIGAVLATKQ-VSEWEKFYEHLPSELEI-----NPSLEALRRMVTLGYNH 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FDRIALLCHLKYLSIGYSSSIYSLPRSIGKLQGLQTLNMPSTYIAALPSEISKLQCLHTL 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 LQGKVVVQVHHLSEYLIEELKEKRYFVVLDDLWILHDWNWINEIAFPKNNKKGSQIVITT 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 WNVDLAEKCAT--ASLVYHLDFLOMNDAITLLLRKTNKNHEDMESNKNMOKMVERIVNKC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSSIGKLIHLKYLSL-YOASVTYLPSSLRNLKSLLYLNL------RINSGQLIN-- 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | : | | | : : | | | : : | | 296 RNDAIHPHCVTFKPELLTHDECWKLLQRIAFSKQKTITGY---IIDKEMVKMAKEMTKHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----LELRYLSLP----WERSSLT
02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                532 VVYNTSIFSGENDMKNSKLRSLLFIPVGYSRFSMGSNFIELPLLRVLDLDGAKFK-GGKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RCSRKFVSDNFSLNHPMKCITNTICLPKVFTPLVSRDDRAIQIAELHMATKSCWYKSFGV
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A, Map position: 1
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|                                                                                                                                                        | Query Match  Query Match  12.9%; Score 663; DB 2; Length 847;  Best Local Similarity 28.9%; Pred. No. 2.2e-34;  Matches 232; Conservative 143; Mismatches 283; Indels 144; Gaps 37;  Qy 73 EDIRNQSAENVDEAEL-VGFSDSKURLL-EMIDTNANDGPAKVICVVGMGGLGK 124                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |

Indels 171;

311;

Mismatches

Conservative 171;

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Matches

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A;Gene: RPP8

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H96617
probable disease resistance protein F9K23.6 [imported] - Arabidopsis thalians
C;Species Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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disease resistance protein RPP8 [validated] - Arabidopsis thaliana
disease resistance protein RPP8 [validated] - Arabidopsis thaliana
disease resistance protein RPP8 [validated] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 21-Jul-2000
C;Accession: T48898
A;Title: Intragenic recombination and diversifying selection contribute to the evolution A;Reference number: 224999; MUID:99030193; PMID:9811794
A;Accession: T48898
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: DNA
A;Residues: 1-906 <ACD>
A;Residues: 1-906 <ACD>
A;Residues: BMBL:AF089710; NID:93928861; PIDN:AAC83165.1; PID:93928862
                                                                                                                                                                                                       PEDFEIKRNRLVGRWIAEGFVRPKVGMTTKDVGESYFNELINRSMIQRSRVGIAGKIKTC 424
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                                                                                                                                                                                                                                                                                                                                                    LTIGAVLATKQVSEWEKFYEHLPSELEINPSLEALRRMVTLGYNHLPSHLKPCFLYLSIF 364
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                                                                                                                                                  AEKCATASLVYHLDFLQMNDAITLLLRKTNKNHBDMESNKNMQKMVERIVNKCGRLPLAI
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Pred. No. 3.6e-34;
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C;Function:
A;Description: promotes resistance to Peronospora parasitica
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LRIEEEAMPSLIKLTVK-GRLE 830
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A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Razzo, M.; Roonley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
A; Scatus: preliminary
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-899 csTO>
A; Cross-references: UNIPROT:Q9C646; GB:AE005173; NID:g11034973; PIDN:AAG27128.1; GSPDB:G
A; Cross-references: UNIPROT:Q9C646; GB:AE005173; NID:g11034973; PIDN:AAG27128.1; GSPDB:G
A; Map position: 1
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                                                                                                                                                                                                                                                   123;
                                                                                                                                                                                                                           DB 2; Length 899;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                459
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TVLDLSYCCLEE-DPMPILEKILELKDLSLDYLSFSGRKがVCSAGGFPQLRKLALDEQEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            resistance protein RPP13 [imported] - Arabidopsis thaliana (resistance protein RPP13 [imported] - Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 02-Sep-2000 C;Accession: T51185
R;Bittner-Eddy, P.D.; Crute, I.R.; Holub, B.B.; Beynon, J.L.
P;Bant J. 21, 177-188, 2000
A;Title: RPP13 is a simple locus in Arabidopsis thaliana for alleles that sA;Reference number: Z25333
A;Reference number: Z25333
A;Accession: T51185
A;Accession: T51185
A;Accession: T51185
A;Accession: T51187
A;Adolecule type: DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EALRRMVTLGYNHLPSHLKPCFLYLSIFPEDFEIKRNRLVGRWIAEGFVRPKVGMTTKDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GESYFNELINRSM---IORSRVGIAGKIKTCRIHDIIRDITVSISROENFVLLPMGDGSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | ||||||| ::|| ARYYIEELIDRSLLEAVRRER----GKVMSCRIHDLLRDVAIKKSKELNF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LREIRFEDGSSPQLEKIEIRFCRLESGIIGIIHLPRLKEISLGYESKVAGLAQLEGEVRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 HGVG----RSNGGPVVGMVASGNQSCLAIDSYAEDIRNQSARNVDEAE-LVGFSDSKKRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LKDMIRQLLGPSS----LDQLLQELQGKVVVQVHHLSEYLIBELKEKRYFVVLDDLWILHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WNWINEIAPPKNNKKGSQIVITTWNVDLAEKCATASLVYHLDFLQMNDAITLLLRKTNKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HEDMESNKNMOKMVERIVNKCGRLPLAILTIGAVLATKQVSEWEKFYEHLPSELEINPSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              454 LVQENTRHIAFHGSMSCKTGLDWSII------RSLAIFGDRPKSLAHAVCPD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -VNVYNDHVAQHSSTTCRREVVHHQVKRYSSEKRKNKRMRSFLNFG-----LDNLVGPDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -QLRMLRVLDLEDVTF-LITQKDFDRIALLCHLKYLSI-GYSSSIYSLPRSIGKLQGLQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 831;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-831 <BIT>
A;Cross-references: EMBL:AF209731; PIDN:AAF42831.1
A;Experimental source: cultivar Rld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VQNIPFIK 896
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Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.-C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Aitle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MuID:21016719; PMID:11130712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable disease resistance protein F9K23.7 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001 C;Accession: G96617
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508 VYNDHVAQHSSTTCRREVVHHQFKRYSSEKRKNKRMRSFLYFGE----FDHLVGLDFETL
                                                                                                                                                                                                                                                 RMLRVLDLEDVTFLITQKDFDRIALLCHLKYLSI-GYSSSIYSLPRSIGKLQGLQTLNMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         621 IQIAELHMATKSCWYKSFGVKVPKGIGKLRDLQVLEYVDIRRTSSRAIK-ELGQLSKLRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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A;Molecule type: DNA
A;Residues: 1-900 <STO>
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C,Superfamily: disease resistance protein RPS2, leucine-rich alpha-2-glycoprotein repeat
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hypotherical protein F12A12.50 - Arabidopsis thaliana
hypotherical protein F12A12.50 - Arabidopsis thaliana
hypotherical protein F12A12.50 - Arabidopsis thaliana
C, Species: Arabidopsis thaliana (mouse-ear cress)
C, Species: Arabidopsis thaliana (mouse-ear cress)
C, Accession: T45590
A, Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Submitted to the Protein Sequence Database, December 1999
A, Reference number: Z23008
A, Accession: T45590
A, Accession: T45590
A, Accession: T45590
A, Residues: 1-835 < CHO>
A, Residues: 1-835 < CHO>
A, Residues: 1-835 < CHO>
A, Residues: Collambia; BAC clone F12A12
C, Genetics:
A, Map Position: 3
                                                                                                                                                                                                                                                                                                                                                                                                        LAMPSIYIAALPSEISKLOCLHILRCSRKFVSDNFSLNHPMKCITNTICLPKVFTPLVSR 616
                                                                                                                       DDRAIQIAELHMATKSCWYKSFGVKVPKGIGKLRDLQVLEYVDIRRTSSRAIKELGQLSK 676
                                                                                                                                                               648 -GDAANLQTLRFISSDSWNK----LKPELLINLRDLEIYEDYD-EDFDRRVSVSWASLTK 701
                                                                                                                                                                                                                                              LRKLGVMTNGSTKEKCKILCAAIEKLSSLQYLYVNAAGISDGGTLECLDSISSPPPLLRT 736
                                                                                                                                                                                                                                                                                737 LVLYGSLEEMPNWIEQLTHLKKIYLLRSKLKEGKTMLILGALPNLMVLDLYRKAYLGEKL 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      797 VFKTGAFPNLRTLSIYDLDQLREIRFEDGSSPQLEKIEIRFCRLESGIIGIIHLPRLKEI 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVSEQFGRLRKLQIFIHNSLDELQIEEEAMPNLIELKITFKEVKKLII-----PNRLRA 925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMIDTNANDGPAKVICVVGMGGLGKTALSRKIFESEEDIRKNFPCNAWITVSQSFHRIEL 159
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                                                           LEV-STY-----SEYPIYDTIDL-RKLT----SLRHVIGQFVGELLI------
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Matches 239; Conservative 128; Mismatches 298; Indels 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 835;
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Pred. No. 1.4e-32;
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28.8%;
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                                                                                                                                                                                                                                                                              AIFGDRPKS---LAHAVCPDQLRMLRVLDLEDVTFLITQKDFDRIALLCHLKYLSIGYSS 539
                                                                                                                                                                                                                                                                                                                                            ITNTICLPKVFTPLVSRDDRAIQIAELHMATKSCWYKSFGVKVPKGIGKLRDLQVLEYVD 659
                                                                                                                                                                                                                                                                                                                                                                                                  ----VCTKSLFVPNCLMGMHELRYLRLPFNTSK------EIKLGLCNLVNLETLENFS 675
                                                                                                                                                                                                                                                                                                                                                                                                                           660 IRRTSSRAIKELGQLSKLRKLGVMTNGSTKEKCK-ILCAAIEKLSSLQYLYVNAAG---- 714
                                                                                                                                                                                                                                                                                                                                                                                                                                         ----ISDGGTLECLDSISSPPPLLRTLVLYGSLEEMPNWIEQLTHLKKIYLLRSKLKEGK 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TMLILGALPNLMVLDLYRKAYLGEKLVFKTGAFPNLRTLSIYDLDQLREIRFEDGSSPQL 830
                                   LWILHDWNWINEIAFPKNNKKGSQIVITTWNVDLAEKCATASLVYHLDFLOMN---DAIT 267
                                                         -----TIAMHGNRRYVNFKPECLT 313
                                                                                   LL-----LRKTNKNHEDMESNKNMQKMVERIVNKCGRLPLAILTIGAVLATKQV-SE 318
                                                                                                                                  WEKFYE----HLPSELEINP-SLEALRRMVTLGYNHLPSHLKPCFLYLSIFPEDFEIKRN 373
                                                                                                                                                                                RLVGRWIAEGFVRPK--VGMTTKDVGESYFNELINRSMIQRSRVGIAGKIKTCRIHDIIR 431
                                                                                                                                                                                                                               DITVSISRQENFV----LLPMGDGSDLVQENTRHIA-----FHGSMSCKTGLDWSIIRSL 482
                                                                                                                                                                                                                                                                                                                            SIYSLPRSIGKLQGLQTLNMPSTYIAALPSEISKLQCLHTLRCSRKFVSDNFSLNHPMKC 599
                                                                                                                                                                                                                                                                                             EKIEIRFC-RLESGIIGIIHLPRLKEISL 858
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| | | : : : : | : : : | SQEFTRKNVWQMILQNLTSRETKDEILQ-
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resistance protein RPP13 [imported] - Arabidopsis thaliana

resistance protein RPP13 [imported] - Arabidopsis thaliana

resistance protein RPP13 [imported] - Arabidopsis thaliana

resistance protein RPP13 [imported] - Arabidopsis thaliana

c;Species - Jul-2000 #sequence_revision 28-Jul-2000 #text_change 09-Jul-2004

c;Accession: T51186

A;Reiture-Reddy, P.D.; Crute, I.R.; Holub, B.B.; Beynon, J.L.

Plant J. 177-188, 2000

A;Reiture-Reddy, P.D.; Crute, I.R.; Holub, B.B.; Beynon, J.L.

A;Reference number: Z25333

A;Reference number: Z25333

A;Residue: preliminary; translated from GB/EMBL/DDBJ

A;Residues: PRDA

A;Residues: 1-820 - SETT>

A;Residues: 1-820 - SETT>

A;Residues: 1-820 - SETT>

A;Residues: 1-820 - SETT>

A;Repidues: 1-820 - SETT>

A;Repidues: 1-820 - SETT>

A;Repiduental source: cultivar Neiderzens
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A;Gene: RPP13 A;Map position: 3 C;Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprotein repeat

34; 779 159 456 507 744 743 174 LKDMIRQLLGPSSLDQLLQELQGKVVVQVHHLSEYLIEELKEKRYFVVLDDLWILHDWNW 219 287 279 - RKDEDLLKTGKEMVQKCRGLPLCIVVLAGLLSRKTPSEWNDVCNSLWRRLK-DDSIHVA 402 565 618 626 704 EMPNWIEQLTHLKKIYLLRSKLKEGKTMLILGALPNLMVLDLYRKAYLGEKLVFKTGAFP 804 280 MESNXNMOKMVERIVNKCGRLPLAILTIGAVLATKOVSEWEKFYEHLPSELEINPSLEAL 339 DLEDVTFLITQKDFDRIALLCHLKYLSI-GYSSSIYSLPRSIGKLQGLQTLNMPSTYIAA 566 653 627 HMATKSCWYKSFGVKVPKGIGKLRDLQVLEYVDIRRISSRAIK-ELGQLSKLRKLGVMTN 685 66 -----YPFLQKMPRLEDLIFENCDYWGGKMSVSEQGFG EMIDTNANDGPAKVICVVGMGGLGKTALSRKIFESEEDIRKNFPCNAWITVSQSFHRIEL 220 INEIAPPKNNKKGSQIVITTWNVDLAEKCATASLVYHLDFLOMNDAITLLLRKTNKNHED RRMVTLGYNHLPSHLKPCFLYLSIFPEDFEIKRNRLVGRWIAEGFVRPKVGMTTKDVGES YFNELINRSM---IQRSRVGIAGKIKTCRIHDIIRDITVSISRQENFVLLPMGDGSDLVQ ENTRHIAFHGSMSCKTG-LDWSI-----IRSLAIFGDRPKSLAHAVCPDQLRMLRVL GSTKEKCKILCAAIEKLSSLQYLYVNAAGISDGGTLECLDSISSPPLLRTLVLYG-SLE 44 HGVG---RSNGGPVVGMVASGNQSCLAIDSYAEDIRNQSARNVDEAE-LVGFSDSKKRLL | : : : : |||||||||||||| : EKL-LDYDEKURFISIFGKGGLGKTALARKLYNS-GDVKRRFEYRAWTYVSQEYKTGDI DLEALL----GPPASNGDLIHLRYLRFDGFSLRVFDIAAIISKSRPLQTLD--ADHVCF 567 LPSEISKLOCLHTLRCSRKFVSDNFSLNHPMKCITNTICLPKVFTPLVSRDDRAIQIAEL IYDTID------LRKFT----SLRH-----VIGKFVGELLIGD--AANLQTL 149; Length 820 Indels 12.3%; Score 631.5; DB 2; 27.7%; Pred. No. 2.2e-32; NLRTLSIYDLDQLREIRFEDGSSPQLEKIEIR 836 | | ::::: | :::: | :::: | :::: | RLRKLKLF-INRLDELQIEEEAMPNLIELVVQ 810 Similarity EDP 100 160 288 340 400 457 999 654 745 744 805 780 Query Match 셤 g q ò g ò g 8 요 ద ò g ద ò 셤 ò g ð 셤 ò 유 8 8 8 8 à 8 ð

hypothetical protein [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004 C;Accession: A86243

Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L. Nature, Also, 2000
Nature, Also, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Maiziali,

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RESULT 14
B96538
hypothetical protein F1413.19 [imported] - Arabidopais thaliana
C;Species: Arabidopais thaliana (mouse-ear crees)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
Chin, C.W.; Edwar, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Jul, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, E.; Kim, C.C., Li, Y.; Aliu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: B86538
A;Accession: B86538
A;Accession: B86538
A;Residues preliminary
A;Residues [1-8] SCTO.
A;Residues [1-8] SCTO.
A;Residues [1-8] SCTO.
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A;Residues [1-8] SCTO.
A;Residues [1-8]
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A;Gene: F1413.19
A;Map position: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VNKCGRLPLAILTIGAVLATKQV-SEWEKFYEHLPSELEINPSLEALRRMVT-----LGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NHLPSHLKPCFLYLSIFPEDFEIKRNRLVGRWIAEGFVRP----KVGMTTKDVGESYFNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VITTWNVDLAEKCATASLVYHLDFLQMNDAITLLLRKTNKNHEDMESN - - KNMQKMVERI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 603.5; DB 2;
Pred. No. 1.4e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.7%; (24.5%; )
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Matches 222; Conserv
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Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
A;Authors: Wu, D.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of Chronosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Referus: preliminary

A;Residus: preliminary

A;Residus: 1-821 <STO>

A;Cross-references: UNIPROT:004093; GB:AE005172; NID:g1931650; PIDN:AAB65485.1; GSPDB:GN

C;Genetics:

A;Map position: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KTCRIHDIIRDITVSISRQENFV-LLPMGDGSDLVQ----ENTRHIAFHGSMSCKTGLDW 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SI---IRSLAIFGDRPKSL---AHAVCPDQLRMLRVLDLEDVTFLITQKDFDRIALLCHL 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YV----NAAGISDGG--TLECLDSISSPPPLLRTLVLYGSLEEMPNWIEQLTHLKKIYLL 762
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                                                                                                                                                                                                                                                                              12.2%; Score 628; DB 2; Length 821;
ilarity 27.5%; Pred. No. 3.7e-32;
Conservative 152; Mismatches 292; Indels 124;
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GSPDB:GN

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| 323 YEHLPSELEINPS-LEALRRMVTLGYNHLPSHLKPCPLYLSIFPEDFEIKRNRLVGRWIA | QY                                                               | QY         544 LPRSIGKLQGLQTLNMPSTY1AALPSBISKLQCLHTLRCSRKFVSDNFSLMHPMKCITNT 603           Db         602 FPRSMBDLHNLQILDASYCQNLKQLQ | 663 TSSRAIKELGQLSKLRKL<br>:                                                                                                                                                                                                                                                                                                                                                                                 | QY         755 HLKKIYLLRSKLKEGKTYMLILGALPNL-MYLDLYRKAYLGEKLVFKTGAFPNLRTLSIYD 813           Db         190 HWRIMLSSLSDLDMDWEVLQQSMPYLRTVTANW 825           QY         814 LDQLREIRPED 824           :                                                                                                                                                                                                                              | Search completed: February 9, 2005, 08:54:50<br>Job time : 33.7041 secs                                                                                                                                                                                                                                                                         |                                                                                                                                                                                                                                                                            |                                                                 |                                                                                                                                           |
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| Db 600                                                           | 738 VLYGSLEEMPNWIEQLTHLKKIYLLRSKLKEGKTWLILGALPNLAWLDLYRKAYLGEKLV | Db 756 CSKNLENLEEWTVEDGAMMRLVTVELKCCNKLKSVPEGTRFLKNLQEV 803  Qy 857 SLGYESK 863  1   1    Db 804 EIGNRTK 810  RESULT 15             | T08416 disease resistance protein homolog F18B3.230 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 11Jun-1999 #sequence revision 11Jun-1999 #text_change 26-May-2000 C;Accession: T08416; S71195 R;Quetier, P:, Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Salanoub submitted to the Protein Sequence Database, May 1999 A;Reference number: Z16409 | A; Accession: T08416 A; Accession: T08416 A; Molecule type: DNA A; Residues: 1-852 < QUE> A; Cross-references: EMBL: AL049862; GSPDB: GN00061; ATSP: F18B3.230 A; Experimental source: cultivar Columbia; BAC clone F18B3 R; Rouse: D.T.; Heazlewood, J.L. submitted to the EMBL Data Library, January 1995 A; Description: Incomplete sequence of an Arabidopsis gene with similarities to myosin he A; Reference number: S71195 | A;ACGEBION: S/1125 A;ACOLGCULE type: DNA A;ROLGCULE type: DNA A;ROLGCULE type: DNA A;ROLGCULE type: DNA A;ROLGCULE type: DNA A;COSS-references: EMBL:U19616; NID:g699494; PID:g699495 C;Genetics: C;Genetics: A;Gene: A7SP:F18B3.230 A;Map position: 3 C;Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprotein repeat | Query Match 11.7%; Score 601.5; DB 2; Length 852; Best Local Similarity 25.0%; Pred. No. 2e-30; Matches 213; Conservative 150; Mismatches 297; Indels 191; Gaps 32;  Qy 28 TSLLLGVEKDIWYLFRHGVGRSNGGPVVGMVASGNQSCLAIDSYAEDIRNQSARNVDEAE 87  On 193 MYRGANDEPPRETTESMYGPDMC | 88 LVGFSDSKKRLLEMIDTNANDGPAKVICVVGMGGLGKTALSRKIFESEEDIRKNFPCNAM | Db 218 VSVSQTFTEEQIMESILEN-LGDASVGDDIGTLIKIQQYLLGRRYLIV 265  Qy 208 LDDLWILHDWN-WINEIAFPKNNKKGSQIVITTWNVDLAEKC-ATASLVYHLDFLQWND 264  :  - |

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Hordeum vulgare (Barley).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
NCBI_TaxID=4513;
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079732 oryza -
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MEDINE=25606637; PubMed=12715163;

MEDINE=25606637; PubMed=12715163;

Madsen L.H., Collins N.C., Rakwalska M., Backes G., Sandal N.,

Krussell L., Jensen J., Waterman E.H., Jahoor A., Pryor A.J.,

Langridge P., Schulze-Lefert P., Stougaard J.;

Langridge P., Schulze-Lefert P., Stougaard J.;

Langridge P., Schulze-Lefert P., Stougaard J.;

Mol. Genet. Genomics 269:150-161(2003).

REMBL; AJ507094; CAD45030.1; -.

REMBL; AJ507094; CAD45030.1; -.

RO; GO:0005224; F.ATP binding; IEA.

GO; GO:0042829; Prèdéense response to pathogen; IEA.

RO; GO:0042829; Prèdéense response to pathogen; IEA.

RICEPRO; IPR002182; NB-ARC.

InterPro; IPR002182; NB-ARC.

InterPro; IPR00518; Wing-lix_DNA_bnd.

Prem; PP00931; NB-ARC; IL BARC.

PREMINTS; PR00364; DISEASERSIST.

SEQUENCE 1014 AA; 114280 MW; 62C3FESF04657332 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
NBS-LRR disease resistance protein homologue.
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45.1%; Score 2319; DB 2;
Best Local Similarity 49.8%; Pred. No. 8.1e-133;
Matches 509; Conservative 149; Mismatches 263;
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Best Local Similarity 48.2%; Pred. No. 1.4e-124;
Matches 488; Conservative 143; Mismatches 279;
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                          EMBL; AP001168; BAA90798.1; -. Gramene; Q9LWW7; -. Gramene; Q9LWW7; -. GO; GO:0005524; F:ATP binding; IEA. GO; GO:0006915; P:aepoptosis; IEA. GO; GO:00042829; P:aefense response to pal InterPro; IPR000767; Disease resist. InterPro; IPR002182; NB-ARC. Flam; P:00931; NB-ARC; 1. PRIMTS; PR00364; DISEASERSIST. SEQUENCE 1007 AA; 114793 MW; F96F2CE
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0MAR-2004 (TrEMBLrel. 26, Last annotation update)
Similar to gene for Pab.
Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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    SRQENFVLLPMGDGSDLVQENTRHIAFHGSMS-----CKTGLDWSIIRSLAIFGDRP 489
                                                                                                                                                                                                                                                                                    TNTICLPKVFTPLVSRDDRAIQIAELHMATK-----SCWYKS---FGVKVPKGIG
                                                                                                                                                                                                                                                                                                                                               KLRDLQVLEYVDIRRISSRAIKELGQLSKLRKLGVMTNGSTKEKCKILCAAIEKLSSLQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 767 KEGKTMLILGALPNLMVLDLYRKAYLGEKLVFKTGAFPNLRTLSIYDLDQLREIRFEDGS
                                                                                                                                                                 KSLAHAVCPDQLRMLRVLDLEDVTFLITQKDFDRIALLCHLKYLSIGYSSSIYSLPRSIG
                                                                                                                                                                                                                                                                                                                                                                                                        708 LYVNAAGISDGGTLE-CLDSISSPPPLLRTLVLYGSLEEMPNWIEQLTHLKKIYLLRSKL
                                              RWIAEGFVRPKVGMTTKDVGESYFNELINRSMIQRSRVGIAGKIKTCRIHDIIRDITVSI
                                                                                                                                                                                                                          550 KLQGLQTLNMPSTYIAALPSEISKLQCLHTLRC-----SRKFVSDNFSLNHPMKCI
                                                                                                                                                                                                                                            Oryza sativa (japónica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 PAC
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EMBL, AP004592; BAC75861.1; -.
Gramene, Q84QL0; -.
GO; GO:0005915; P:ATP binding; IEA.
GO; GO:0005915; P:apoptosis; IEA.
GO; GO:0042829; P:defense response to pathogen; IEA.
InterPro; IPR00167; Disease_resist.
InterPro; IPR001611; LRR.
InterPro; IPR001812; NB-ARC.
PF00560; LRR_1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome
clone:P0666G10.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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 Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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Name=P0666G10.123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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0840L0;
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------DEAEL-VGFSDSKKRLLEMIDTNANDGPAKVICV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DQLLQELQGKVVVQVHHL----SEYLIEELKE----KRYFVVLDDLWILHDWNWI 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KTI-PPENS--SSRIIVTTRPKLVAQHCSEEEEYMARIGDLKDKDALDLFLDKFLIYLFG 852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 V---GMGGLGKTALSRKIFESEEDIRKNFPCNAWITVSQSFHRIELLKDMIRQLLGPSSL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----TNKNHED------MESNKMMQKMVERIVNKCGRLPLAILTIGAVLATK--QVS 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     853 NYKVCKKGDESELKPDMMDILKKNPDMIAEAELIVKKCGRLPLAIVAVGGFLSTRPPNIR 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EWEKFYEHLPSELEINPSLEALRRMVTLGYNHLPSHLKPCFLYLSIFPEDFEIKRNRLVG 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 YLFRHGVGRSNGGPVVGM-----VASGNQSCLAI-----DSYAEDIRNQSARNV-- 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LDQLREIRFEDGSSPQLEKIEIRPCRLESGIIGIIHLPRLKEISLGYESKVAGLAQLEGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                       Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                       VRTHPNHPVLRKREDRSDHDLACDA-----EGSPVEVEATDPLPEQEGESSQ 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 22.8%; Score 1172; DB 2; Length 1485; Best Local Similarity 33.9%; Pred. No. 1.6e-62; Matches 326; Conservative 163; Mismatches 312; Indels 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                      PAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0364; DISEASERSIST.
PROSITE; PS00136; SUBTILASE ASP; UNKNOWN 1.
SEQUENCE 1485 AA; 167594 WW; 181AB09G7BAB8006 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone:P0666G10.";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                      chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AP004552; BAD33147.1; -...

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0006515; P:apoptosis; IEA.

GO; GO:00042825; P:defense response to pathogen; IEA.

InterPro; IPR00076; Disease_resist.

InterPro; IPR001611; IRR.

InterPro; IPR000209; Pept S8 S53.

Pfam; PF00560; IRR_1; 2.
                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                            PRT; 1485 AA
                                                                                                                                                                                                                                                                                                                                                                                                                    Sasaki T., Matsumoto T., Yamamoto K.; "Oryza sativa nipponbare(GA3) genomic DNA,
                                                                                                                                                                                                                                      25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                   Putative Pi-b protein.
Name=P0666G10.130;
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PibH8 protein.
                                      Name=PibH8;
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                                                          24;
                                                                                       522 PGLARSGLSTMGSEELIDKLKODLTGKKYLIVLDDLSTTTEWDSIIR-NLPINN-NGSRI 579
                                                                                                                                                                                                         NLRTLSIYDLDQLREIRFEDGSSPQLEKIEIRFCRL--ESGIIGIIHLPRLKEIS-LGY- 860
                                                                                                                                     521
                                                                                                                                                                                                                                     NKCGRLPLAILTIGAVLAT--KQVSEWEKFYEHLPSELEINPSLEALRRMVTLGYNHLPS 352
                                                                                                                                                                                                                                               640 KKCGRLPLAVATVGGFLSARPRNIEWREFSDRISEEFDNNPSLEMIKKILASSYEGLTY 699
                                                                                                                                                                                                                                                                           HLKPCFLYLSIFPEDFEIKRNRLVGRWIAEGFVRPKVGMTTKDVGESYFNELINRSMIQR 412
                                                                                                                                                                                                                                                                                                                 SRVGIAGKIKTCRIHDIIRDITVSISRQENFVLLPMGDGSDLVQENTRHIAFHGSMSCKT 472
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                                                                                                                                                                                              VITTWNVDLAEKCATASL-VYHLDFLQMNDAITLLLRKTNKNHEDMESNKNMQKMVERIV 294
                                                                                                                                                                                                                                                                                                                                                       G----LDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLEDVTFLITQKDFDRIALL 527
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                                                                            RNOSARNVDE----AELVGPSDSKKRLLEMI-DTNANDGPAK-VICVVGMGGLGKTALS
                                                                                                                  RKI FESEEDIRKNFPCNAWITVSQSFHRIELLKDMIRQLLGPSSLDQLLQELQGKVVVQV
                                                                                                                               935 EDDOPIIKLLHOFRSIREEMGTRFAVSYIMLFIT---------
                                                                                                                                                        HHL------SEYLIEELKE----KRYFVVLDDLWILHDWNWINEIAFPKNNKKGSQI
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                                                          Gaps
                                     Query Match 21.4%; Score 1101.5; DB 2; Length 1226; Best Local Similarity 33.3%; Pred. No. 2.5e-58; Matches 288; Conservative 165; Mismatches 299; Indels 113;
                    CRC64;
                    F45F3EBCF9F0251A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --ESKVAGLAQLEGEVRTHPNHPVL
                    138086 MW;
Pfam; PF00931; NB-ARC; 1.
PRINTS; PR00364; DISEASERSIST.
SEQUENCE 1226 AA; 138086 MW
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PRELIMINARY;

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RESULT 5 Q9MBF2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236 VITTWNVDLAEKCATASL-VYHLDFLQMNDAITLLLRKTNKNHEDMESNKNMQKMVERIV 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRVGIAGKIKTCRIHDIIRDITVSISRQENFVLLPMGDGSDLVQENTRHIAFHGSMSCKT 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGLARSGLSTWGSEELIDKLKQDLTGKKYLIVLDDLSTTTEWDSIIR-NLPINN-NGSRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Tohoku IL-9; TISSUE-Green leaf; MEDLINE-99348180; PubMed-10417726; Mang Z., Yano M., Yamanouchi U., Iwamoto M., Monna L., Hayasaka H., Katayose Y., Sasaki T.; "The Pib gene for rice blast resistance belongs to the nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Toloku II-9; TISSUB=Green leaf;

X MEDLINE=21582385; PubMed=11725950; DOI=10.1023/A:1012457113700;

A WEDLINE=21582385; PubMed=11725950; DOI=10.1023/A:1012457113700;

A WEDLINE=21582385; PubMed=11725950; DOI=10.1023/A:1012457113700;

A WEDLINE=21582385; PubMed=11725950; DOI=10.1023/A:1012457113700;

A WEDLINE=215823821; PubMed=11725959; DOI=10.1023/A:1012457113700;

A ROY GO:0005915; Papple First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First First F
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Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
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SEQUENCE 1226 AA; 138086 MW; F45F3EBCF9F0251A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The Pib gene for rice blast resistance belongs to the binding and leucine-rich repeat class of plant disease
Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000767; Disease_resist.
InterPro; IPR001611; LRR.
InterPro; IPR002182; NB-ARC.
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Matches 288; Conservative 165;
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Pfam; PF00931; NB-ARC; 1
01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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349 KMQ--RLSDAASRELFFKRIFGSADISSNEELDEVSNSILKKCGGLPLAIVSIGSLVASK 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DITVSISROENFVLLPMGDGSDLV-QENTRHIAFHGSMSC--KTGLDWSIIRSLAIFGDR 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNRLVGRWIAEGFVRPKVGMTTKDVGESYFNELINRSMIQRSRVGIAGKIKTCRIHDIIR 431
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                                                                                                                   | : | : | : | : | : | : | : | : | CTFNIRTLEQYMIRELIORPNXAMAVAGGKHGHTMDGNMDGMERWEVAVLAEKVRQYLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVIISKSLEENPASFLCDNGHPLVCHDKIRRLSIHNSHNSVORTRVSVSHVRSFTM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PKSLAHAVCP---DQLRMLRVLDLEDVTFLITQKDFDRIALLCHLKYLSIGYSSSIYSLP
                       DEPRDKLVRWV--MEADPCRRVLAIVGFGGLGKTTLARMVCENPMVKGADFHCCPLFIVS
                                                                                                                                                                                                              HLDFLQMNDAITL-LLRKTNKNHEDMESNKNMQKMVERIVNKCGRLPLAILTIGAVLATK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --SASVEBUPMFFPQMRLLKVLDLQGSSCL-NNSTLNYICKFYQLKYLTL-RKTNIGKLP
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SDSKKRILLEMIDTNANDGPAKVICVVGMGGLGKTALSRKIFESEEDIRKNFPCNAWITVS
                                                                                           QSFHRIBLLKDMIRQLL-GPS-----SLDQLLQBLQ-GKVVVQVHHLSEYLIE
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                                                                                                                                                                                   ELKEKRYFVVLDDLWILHDWNWINEIAFPKNNKKGSQIVITTWNVDLAEKCATA--SLVY
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to NBS-LRR type resistance gene.
Name=P0702F05.14;
Name=P0702F05.14;
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMPNWIEQLTHLKKIYLLRSKLKEGKTMLILGALPNLMVLDLYRKAYLGEKLVFKTGAFP 804
                                                  875 HHLKYLSLRGSFGVFNLPNSFGNLLNLETLDIRGTWVTKLPATIGRLONLKYVHAGSLDD 934
                                                                                                                                                                                                         -----CLHTLRCSRKFVSDNFSLNHPMKCITNTICLPKVFTPLVSRDDRAIQIAELH 627
                                                                                                                                                                                                                                                                                               628 MATKSCWYKSF---GVKVPKGIGKLRDLQVLEYVDIRRTSSRAIKELGQLSKLRKLGVMT 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 HDTQVRIWMKQVREIAYDAEDCIDQFTHHLGESSG---IGFLYRLIYILGKLCCRHRIAM 117
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                                                                                                                                                                                                                                   NLRTLSIYDLDQLREIRFEDGSSPQLEKIEIRFCRL--ESGIIGIIHLPRLKEIS-LGY-
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                                                                                                              CHLKYLSIGYSSSIYSLPRSIGKLQGLQTLNMPSTYIAALPSEISKLQ------
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
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llarity 29.3%; Pred. No. 1.9e-56;
Conservative 194; Mismatches 333; Indels 180;
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Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005828; BAD46438.1; -.
SEQUENCE 953 AA; 108557 MW; DAFD5081E707261C CRC64;
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Sabaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
Similar to NBS-LRR type resistance gene.
Name=P0702F05.17;
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nes 293; Conserv
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 837 PNLLCLKLYHKSYADNCIVFCHGKFVKLKLIIDNLERIEKMQFDAGSVTNLERLTLSFL 896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 NAWITVSQSFHRIELLKDMIRQLLGPSSLDQLLQELQGKVVVQVHHLSEYLIEELKEKRY 204
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                                                                                                                                                                                                                                                        Eukaryota; Viridinimae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                           R PubMed=14645721; DOI=10.1073/pnas.2435133100;
A Feuillet C. Travella S., Stein N., Albar L., Nublat A., Kell "Map-based isolation of the leaf rust disease resistance gene from the hexaploid wheat (Triticum aestivum L.) genome.";
L From the hexaploid wheat (Triticum aestivum L.) genome.";
L From the hexaploid wheat (Triticum aestivum L.) genome.";
R GOI, Natl. Acad. Sci. U.S.A. 100:15253-15258(2003).
R GOI, GO:000524; F:ATP binding; IEA.
R GO; GO:000524; F:ATP binding; IEA.
R GO; GO:000524; F:ATP binding; IEA.
R GO; GO:000524; P:apoptosis; IEA.
R GO; GO:0006315; P:apoptosis; IEA.
R InterPro; IPR000161; LRR.
R InterPro; IPR001611; LRR.
R InterPro; IPR001611; LRR.
R InterPro; IPR001822; NB-ARC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131589 MW; A64E186A3664C6CA CRC64;
                              R-LESGIIGIIHLPRLKEISLGYESKVAGLAQLEGEVRTHPNHP | : | | | : : | : | : | | | | | | | REPKYGISGLENLPKLKEIEFFGDIILSVVTKVASCVKAHPNHP
                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Resistance protein Tlorga2-1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 20.3%; Score 1042; DB 2;
Best Local Similarity 34.4%; Pred. No. 9.9e-55;
Matches 290; Conservative 159; Mismatches 285;
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SEQUENCE 1169 AA; 131589 MF
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                                                                                                                                                PRELIMINARY;
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Pfam; PF00931; NB-ARC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KINRIKEEWQKVCNNLGSELENNPILEGVKQVLTLSYNDLPYHLKACFLYLSIFPENYVI 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------VQLT--RTASVKFLRQSSGLEVATGVVKNWALQSLVHI-V 718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             K---QVSEWEKFYEHLPSELBINPSLEALRRMVTLGYNHLPSHLKPCFLYLSIFPEDFEI 370
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                                                                                                                                                    Gaps
                                                                                                                                                187;
                                                                                                                Length 954;
                  PAC
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Matches 293; Conservative 182; Mismatches 342; Indels
                  chromosome 6,
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, clone: P0702PSG.";
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
                                                               EMBL, AP005828; BAD46435.1; -.
SEQUENCE 954 AA; 108010 MW; 0F8BEBBE635D2750 CRC64;
                                                                                                                DB 2;
                                                                                                              20.3%; Score 1043.5; 29.2%; Pred. No. 6e-5
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                                                410 IQRSRVGIAG--KIKTCRIHDIIRDITVSISRQENFVLLPMGDGSDL-VQENTRHIAFHG
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       CLAIDSYAEDIRNOSARNVD-----EAELVGFSDSKKRLLEMIDTNANDGPAKVICVV
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Oryza sativa (Rice).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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BMBL; AF326781; AAK84082.1; -. GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:00043829; P:defense response to pathogen; IEA.

Interpro; IPR000767; Disease_resist.
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Bukaryota, Viridiplantea; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
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Wicker T., Stein N., Albar L., Feuillet C., Schlagenhauf E.,
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Pfam; PF00931; NB-ARC; 2
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                                                               SRDDRAIQIABLHMATKSCW-----YKSFGVKVPKGIGKLRDLQVLEYVD
                                                                                                                                                 564 IAALPSEISKLQCLHTLRCSRK--FV-SDNFSLNHPMK---CITNTICLP---KVFTPLV
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                            LRVLDLEDVTFLITQKDFDRIALLCHLKYLSIGYSSSIYSLPRSIGKLQGLQTLNMPSTY
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Name=OJ1634_B10.108;

Oryza sativa (japonica cultivar-group).

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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TICRFAMB; TICR00756; PPR; 4.
SEQUENCE 1494 AA; 168313 MW; 15BB15F247C3446B CRC64;
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"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7,
clone:OJ1634 B10.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005915; P:apptoais; IEA.
GO; GO:0042829; P:adefense response to pathogen; IEA.
InterPro; IPR000767; Disease_resist.
InterPro; IPR001611; IRR.
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Last annotation update)
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InterPro; IPR008940; Prenyl_trans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 MIRQL-LGPSSLDQLLQ----BLQGKVVVQVHHLSEYLIEELKEKRYFVVLDDLWILHDW 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     393 TKDVGESYFNELINRSMI---QRSRVGIAGK-IKTCRIHDIIRDITVSISRQENFVLLPM 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARSLVGSAISKAASAAADETSLL----LGVEKDIWYLFRHG--VGRSNGGPV----VGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                  SEQUENCE FROM N.A.
STRAIN=Tohoku IL-9; TISSUE-Green leaf;
MEDLINE=99348180; PubMed=10417726;
MEDLINE=99348180; Vano M., Yano M., Yano M., Yano M., Yano M., Yano M., Yano M., Yano M., Monna L., Hayasaka H. Katayose Y., Sasaki T.;
"The Pib gene for rice blast resistance belongs to the nucleotide binding and leucine-rich repeat class of plant disease resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 20.1%; Score 1033; DB 2; Length 1251; Best Local Similarity 31.4%; Pred. No. 3.9e-54; Matches 308; Conservative 184; Mismatches 354; Indels 136;
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=BL-1; TISSUB-Green leaves;
Jwa N., Tsunoda Y., Akiyama K., Nakamura S., Motomura T., J
Wodama O., Kawasaki S.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
BMBL; AB013449; BAA76282.2;
BMBL; AB013448; BAA76281.2;
BMBL; AB01348; BAA76281.2;
Gramene; QSSXV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00560; LRR i; 2.
Pfam; PF00931; NB-ARC; 2.
PRINTS; PR00364; DISEASERSIST.
SEQUENCE 1251 AA; 141638 MW; 011F56630118AB98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0006915; P:apoptosis; IEA.
GO; GO:0042829; P:defense response to pathogen; IEA.
InterPro; IPR000767; Disease_resist.
InterPro; IPR001611; IER.
InterPro; IPR001813; NB-ARC.
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                      Plant J. 19:55-64 (1999).
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                               NCBI_TaxID=4530;
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GO; GO:00
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 32,
                                                                                     633
                                                                                                                       86 AELVGPSDSKKRLLEMIDTNANDGPAKVICVVGMGGLGKTALSRKIFESEEDIRKNFPCN 145
                                                                                                                                                                                                          GIAGKIKTCRIHDIIRDITVSISRQENFVLLPMGDGSDLV-QENTRHIAFH--GSMSCKT 472
                                                                                                                                                               AWITVSQSFHRIELLKDMIRQL------LGPSSLDQLLQELQGKVVVQVHHLS 192
                                                                                                                                                                                                                                       EYLIEELKEKRYFVVLDDLWILHDWNWINEIAFPKNNKKGSQIVITTWNVDLAEKCATAS 252
                                                                                                                                                                                                                                                   253 LVYHLDFLQMNDAITLLLRKTNKNHEDMESN-------KOMQKAVERIVNKCG 298
                                                                                                                                                                                                                                                                                                                            299 RLPLAILTIGAVLATKQVSE---WEKFYEHLPSELEINPSLEALRRMVTLGYNHLPSHLK 355
                                                                                                                                                                                                                                                                                                                                        PCFLYLSIFPEDFEIKRNRLVGRWIAEGFVRPKVGMTTKDVGESYFWELINRSMIQRSRV 415
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                                                                                                                                                                                                                                                                                                     -----PHEYDRAYEI-----KPLTDCESRDLFFKRIFGSSICPEHLEDISAKILGKCG 911
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                                    574 CGKQVKIWKKHVREIAYDIEDCIDEFKHQLGDSSSAGGSGPVVFFRKATHILQTTRVRHQ
                                                                                                         -----DE GMVASG--NOSCLAIDSYAEDIRNOSARNV----DE
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 Gaps
 219;
 347; Indels
                    1 MAETVLSMARSLVGSAISKAASAAADETSLLLGVEKDIWYL-----
                                                                ----FRHGVGRSN----GGPVV
174; Mismatches
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 Conservative
306;
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RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y., RA, Nimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H., Hosokawa S., Maeukwa M., Arikawa K., Chiden Y., Hayashi M., Antonio B.A., Kanamori H., Ancamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C., Hijshita S., Honda M., Ichikawa Y., Idonuma A., Iljima M., Ikeda M., Ranasawa W., Katagiri S., Itoh T., Itoh Y., Iwabuchi A., Kamiya K., Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I., Machita K., Machara T., Mizuno H., Mizubayashi T., Mukai Y., Nakamiti N., Negishi M., Okara I., Ono N., Saji S., Sakai, K., Shibata M., Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tauji K., Wani H., Indo H., Indo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y., Yama Shimokawa T., Sologuri T., Ito H., Hahn J.H., Kim H.I., Eun M.Y., The genome sequence and diructure of rice chromosome 1.";

Nature 420.312-316.20021.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELQGKVVVQVHHLSEYLIEELKEKRYFVVLDDLWILHDWNWINEIAFPKNNKKGSQIVIT 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 GRLPLAILTIGAVLA---TKQVSEWEKFYEHLPSELEINPSLEALRRMVTLGYNHLPSHL 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63
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01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Similar to Oryza sativa gene for Pib.
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 19.6%; Score 1005; DB 2; Length 935; Best Local Similarity 31.5%; Pred. No. 1.3e-52; Matches 289; Conservative 179; Mismatches 304; Indels 146;
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A; 104616 MW; AAA0141D63391E83 CRC64;
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GO:0006915; P:apoptosis; IEA.
GO:0042829; P:defense response to pathogen; IEA
                                    935 AA
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InterPro; IPR001611; LRR.
InterPro; IPR002182; NB-ARC.
Plam; PR00560; LRR 1; 2.
Pfam; PR00931; NB-ARC; 2.
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GIILYRYIVILDDIWSSSAWESI-KCAFP-DNKKGSRIIVTTRNEDVANTCCRPQDRI 379
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                                                                                                                                                                                                                                 ATK---QVSEWEKFYEHLPSELEINPSLEALRRMVTLGYNHLPSHLKPCFLYLSIFPEDF 368
                                                                                                                                                                                                                                                                                                                        EIKRNRLVGRWIAEGFVRPKVGMTTKDVGESYFNELINRSMIQRSRVGIAGKIKTCRIHD 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLEYVDIRRISSRAIKELGQLSKLRKLGVMTNG---STKEKCKILCAAIEKLSSLQYLYV 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | :|:|: | :| :| | |||| | : | ::| | : | : | | SLVHVEIKEHPS-VFQEIALLQNLRKLSVLFYGIEVNWKPFLELLNMLSGSVRSLSIDIF 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAAGISDGGTLECLDSISSPPPLLRTLVLYGSLEEMPNWIEQLTHLKKIYLLRSKLKEGK 770
                                                                                                                                          LLRELIQRPRKAMPAVAAAGGGGGDLVAYDALQGMERWETAALASKAEGIPARQKFVHIC 321
                                                                                                                                                                                                                                                                                             ASKPNRSKEEWQKVCDNLGSELESNPTLEGTKQVLTLSYNDLPYHLKACFLYLSIFPENH 497
                                                                                                                                                                                                                                                                                                                                                                         IIRDITVSISROENFVLLPMGDGSDLV-QENTRHIAFHGSMSCKTGLDWSIIRSLAIFGD 487
                                                                               IGYSSSIYSLPRSIGKLOGLOTLNMPSTYIAALPSEISKLOCLHTLRCSRKFVSDNFSLN
             -VDEAELVGFSDSKKRLLEMIDT
                                     DAGERRTRYGVSLAAAAVRGGGGSSSSGRLDPRLHALFTBEAQLVGIDGPREELVGWV--
                                                               NANDGPAKVICVVGMGGLGKTALSRKIFESEE-DIRKNFPCN-AWITVSQSFHRIELLKD
                                                                                                                                                                    EELKEKRYFVVLDDLWILHDWNWINEIAFPKNNKKGSQIVITTWNVDLAEKCA--TASLV
                                                                                                                                                                                                                                                                                                                                     RPKSLAHA----VCPD-----QLRMLRVLDLEDVTFLITQKDFDRIALLCHLKYLS
                                                                                                                                                                                                                                                                                                                                                                                                                                          HPMKCITNTICLPKVFTPLVSRDDRAIQIAELHMATKSCWYKSFGVKVPKG-IGKLRDLO
                                                                                                                                                                                                                    YHLDFLQMNDAITLLL---RKTNKNHEDMESNKNMQKMVERIVNKCGRLPLAILTIGAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TMLILGALPNIMVLDLYRKAYLGEKLVFKTGAFPNLRTLSIYDLDQLREIRFEDGSSPQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-0CT-2004 (TrEMBLrel. 28, Created)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Putative resistance protein.
Name=OSJNBD0034812.23;
Oryza sativa (japonica cultivar-group).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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              DIRNOSARN-
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                                                                                                                                                                                                                                 FVSDNFSLNHPMKCITNTICLPKVFTPLVSRDDRAIQIAELHMATKSCWYKSFGVKVPKG 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | | | | | | | | | : : : | | | | | : : | | | | SHPAAAAGDEGRLVASLRRFV-RLLAGALG------VGGGDRSVAAQLRELKARAR 143
                                         VGIAGKIKTCRIHDIIRDITVSISRQENFVLLPMGD-----GSDLVQENTRHI--AFHG 466
                                                                                                                                            LYLLRYVSL-RSTNISKLPRAVGNLKELLTLDVRSTYIRELPATITQLRCLKHLLAGRYK 653
                                                                                                                                                                                                                                                                                   IGKLRDLQVLEYVDIRRTSSRAIKELGQLSKLRKLGVMTNGSTKEKCKILCAAIEKLS-S 704
                                                                                                                                                                                                                                                                                                                                     LOYLYVNAAGISDGGTLECLDSISSPPPLLRTLVLYGSLEEMPNWIEQLTHLKKIYLLRS 764
                                                                                                                                                                                                                                                                                                                                                    KLKEGKTMLILGALPNLMVLDLYRKAYLGEKLVFKTGAFPNLRTLSIYDLDQLREIRFED 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGLPLAIVSIGGMLARMKNKTYAEWQKVCDRLDCGLEINNTVGGMRKILSLGYNDLPYHL 421
                                                                                         SMSCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLEDVTFLITQKDFDRIAL
                                                                                                                                                                                                                                                                                                 SKAASAAADETSLLLGVEKDIWYLFRHGVGRSNGGPVVGMVASGNQSCLA---IDSYAE
                                                                                                                                                                                                                                                                                                                                                                                                                                         GSSPQLEKIEIRFCRL-ESGIIGIIHLPRLKEI----SLGYESKVAGLAQLEGEVRTHPNH
                          KPCFLYLSIFPEDFEIKRNRLVGRWIAEGFVRPKVGMTTKDVGESYFNELINRSMIQRSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               159;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.3%; Score 992.5; DB 2; Length : llarity 30.5%; Pred. No. 8.2e-52; Conservative 170; Mismatches 333; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             è,
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Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005828; BAD46437.1; -.
SEQUENCE 989 AA; 109590 WW; 09BF11AAD9C3028A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to NBS-LRR type resistance gene.
Name=P0702F05.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  989 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sasaki T., Matsumoto T., Yamamoto K.; "Oryza sativa nipponbare(GA3) genomic DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           896
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290; Conserv
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Pubmed=12447438; DOI=10.1038/nature01184;
Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
A. U., Nilmura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
A. Hosokawa S., Masukawa M., Arikawa K., Hamada M., Harada C.,
A. Hosokawa S., Hond T., Aoki H., Arita K., Hamada M., Harada C.,
A. Hijishita S., Hond M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
Ikeno M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
A. Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
Angasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
Namiki N., Negishim M., Ohta I., Ono N., Saji S., Sakai, K., Shibata M.,
Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tauji K.,
Maki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Bun M.Y.,
Yano M., Jiang J., Gojobori T.,
"The genome sequence and structure of rice chromosome I.";
                                                                                               GKTMLILGALPNLMVLDLYRKAYLGEKLVFKTGAFPNLRTLSIYDLDQLREIRFEDGSSP 828
                                                                                                                                                                                                                                                                                                              QLEKIEIRFCR--LES--GIIGIIHLPRLKEISLGYESKVAGLAQ-LEGEVRTHPNHP 881
                                                                             RDLQVLEYVDIRRISSRAIKELGQLSKLRKLGVMTNGSTKEKCKILCAAIEKLSSLQYLY
                                                                                                                                               710 VNAAGISDGGTLECL-DSISSPPPLLRTLVLYGSLEEMPNWIEQLTHLKKIYLLRSKLKE
                                        --LIHKVEQP--ETDNRKANQLGNM----LSCLYCNSSDYCGISSLDRVSVRAPEGVEKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2004 (TrEMBLrel. 26, Last annotation update)
51milar to Oryza sativa gene for Pib.
Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group).
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Ehrhartoideae; Oryzea, Oryza, Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.8%; Score 965; DB 2; 31.3%; Pred. No. 4.1e-50;
       503 TICLPKVFTPLVSRDDR-AIQIAELHMATKSCWY
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PROSITE; PS00053; RIBOSOMAL SB; UNKNOWN 1.
SEQUENCE 1011 AA; 114012 WW; 14EDDBBA:
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G0; G0:0005524; F:ATP binding; IEA.
G0; G0:0006915; P:apoptosis; IEA.
G0; G0:0042829; P:defense response to pa
InterPro; IPR00167; Disease_resist.
InterPro; IPR001611; LR.
InterPro; IPR001630; NB-ARC.
InterPro; IPR000630; Ribosomal_S8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AP001073; BAA89580.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00560; LRR 1; 2.
Pfam; PF00931; NB-ARC; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ADDTVRTWVKQVRDLAYDVEDSLLDFALFADTLSSSSSSSWWLPWRIAERHRVAARIREL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 KASVEELNORFLRYRIVVEHPRASRGGG----ASDDQQQL----HDHDGQYYSAELAFQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EAELVGFSDSKKRLLEMIDTNANDGPA-----KVICVVGMGGLGKTALSRKIFESEEDI 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231 LDAFDCDAWVTVP---HPLD------SADEFVRRLRRHLAVGKDQDVH---- 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --SLVYHLDFLOMNDAITLLLRKTNKNHEDMESNKNMOKMVERIVNKCGRLPLAILTIGA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        || | | : | : | : | | Helpinary | | GHGHVYELRPLGRESKOLFCQKVYKSTEY1-LEKEMEDLAGPILKRCRGLPLAISTIGG 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 RKNPPCNAWITVSQSFHRIELLKDMIRQLLGPSSLDQLLQELQGKVVV----QVHHLSEY 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              195 LIBELKEKRYFVVLDDLWILHDWNWINEIAFPKNNKKGSQIVITTWNVDLAEKCATA--- 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310 VLATKOVS--EWEKFYEHLPSELEINPSLEALRRMVTLGYNHLPSHLKPCFLYLSIFPED 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              368 FEIKRNRLVGRWIAEGFVRPKVGMTTKDVGESYFNELINRSMIQ--RSRVGIAGKIKTCR 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     426 IHDIIRDITVSISRQENFVLLPMGDGSDLVQENTRHIA---FHGSMSCKTGLDWSIIRSL 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           483 AIFGDRPKSLAHAVCPDQLRMLRVLDLEDVTFLITQKDFDRIALLCHLKYLSIGYSSSIY 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLPRSIGKLOGLOTLNMPSTYLAALPSEISKLOCLHTLRCSRKFVSDNFSLNHPMKCITN 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       619 KLP-SFQNLRYLETLDIQDTKVTQLPDGIAKLEKLRYL----LAGVNFSKE----- 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47
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                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAETVLSMARSLVGSAISKAASAAADETSLLLGVEKDI-------
                                                                                                                                                                                                                                                                                                                                                                                                                  211;
                                                                                                                                                                                                                                                                                                                                                                           Query Match
19.2%; Score 987.5; DB 2; Length 963;
Best Local Similarity 29.8%; Pred. No. 1.6e-51;
Matches 303; Conservative 180; Mismatches 324; Indels 211;
                                                                                                            BAC
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                      Sasaki T., Matsumoto T., Katayose Y.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 9,
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 9,
"Oryza subbolasali.";
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; APO05735; BAD33830.1; -.
GO; GO:0005224; F:ATP binding; IEA.
GO; GO:0006915; P:apoptoals; IEA.
GO; GO:0042829; P:defense response to pathogen; IEA.
InterPro; IPR001631; LRR.
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Pfam; PF00931; NB-ARC; 1.
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                                    NCBI_TaxID=39947;
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Search completed: February 9, 2005, 08:47:56 Job time : 126.246 secs

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Sequence 7, Appli
Sequence 16, Appli
Sequence 6, Appli
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Sequence 111, App
Sequence 109, App
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APPLICANT: Yano, Masao
APPLICANT: Iwamoto, Masao
APPLICANT: Katayose, Yuichi
APPLICANT: Sadaki, Takuji
APPLICANT: Samanouchi, Utako
APPLICANT: Yamanouchi, Utako
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Pred. No. 3.7e-92;
                                               US-09-803-286A-9
US-09-803-286A-6
US-09-004-838-101
US-09-004-838-111
US-08-310-912A-109
US-08-310-912A-109
US-09-301-085-109
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ZIP: 02110-2804

ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDLUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: RastSEG for Windows Version 2.0
SOFTWARE: 1000 DATA:
APPLICATION DATA:
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APPLICATION PROFEMATION:
ATTORNEY/AGENT INFORMATION:
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US-09-357-206A-3
US-09-813-742A-3
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REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 06501/032001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-6976
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1205 amino acids
TYPE: amino acid
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Best Local Similarity
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Sequence 18,
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Sequence 5,
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Sequence 3,
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                            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-310-956A 8
US-09-366-186-3
US-08-310-956A-4
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US-09-316-96B-2
US-09-935-176-5
US-09-935-176-3
US-09-935-176-3
US-09-203-266-2
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US-09-245-928A-19
US-09-245-928A-18
US-09-245-928A-18
US-09-245-928A-18
US-08-34-928A-18
US-08-94-91-912A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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PCT-US95-04589-2
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Maximum Match 100%
Listing first 45 summaries
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308; Conservative 184; Mismatches 354; Indels 136;
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SELECTIVE BREEDING OF TOMATO AND RELATED PLANTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,996A
FILING DATE: 09-DEC-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
16.5%; Score 848; DB 3; L
Best Local Similarity 27.9%; Pred. No. 4.7e-74;
Matches 282; Conservative 173; Mismatches 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 MARSLVGSAISKAASAAADETSLLLGVEKDIWY----
                                                                                                                                                                                                                            Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US96/05272
FILING DATE: 15-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1L 113,373
FILING DATE: 13-APR-1995
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                  B: BROWDY AND NEIMARK
419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                               TYPE: Floppy disk
SR: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 920 amino acids
amino acid
ORI, Naomi
PARAN, Ilan
ZAMIR, Daniel
                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Flonov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                            APPLICANT: ZAMIR, DATITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
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                                                                                                                                                 PKVGMTTKDVGESYFNELINRSMI - - - QRSRVGIAGKIKTCRIHDIIRDITVSISRQENF 443
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                    600 SLIMLRYLSL-FSYGNFDVPPBICRLWNLQTFIVQRFRSDIIIFABEIWBLMQLRHLKLP
LDDLWILHDWNWINEIAFPKNNKKGSQIVITTWNVDLAEKCATASLVYHLDFLQMNDAIT
                                                                                                                              PSELEINPSLEALRRMVTLGYNHLPSHLKPCFLYLSIFPEDFEIKRNRLVGRWIAEGFVR
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                                                                                  PNHPVLRK---REDRSDHDLACDAEGSPVEVEATDPLPEQEGESSQ 920
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APPLICANT: Stankawicz, Douglas
APPLICANT: Dahlbeck, Douglas
APPLICANT: Dahlbeck, Douglas
APPLICANT: Dahlbeck, Douglas
APPLICANT: Tai, Thomas H
TITLE OF INVENTION: B82 RESISTANCE GENE
FILE REFERENCE: 42250/214021 (5830-4A)
CURRENT APPLICATION NUMBER: US/09/864,680A
FRIOR APPLICATION NUMBER: US 09/360,186
FRIOR APPLICATION NUMBER: US 60/093,957
PRIOR APPLICATION NUMBER: US 60/093,957
PRIOR PILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/09864680A; Patent No. 6762285; GENERAL INFORMATION:
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                                                                VRPKVGMTTKDVGESYFNELINRSMIQRSRVGIAGKIKTCRIHDIIRDITVSISRQENF- 443
                                                                                                                              -VLLPMGDGSDLVQ--EN--TRHIAFHGSMSCKTGLDWSIIRSLAIFGDRPKSLAHAVCP 498
                                                                                                                                                 DVYNDDSDGDDAAETWENYGSRHLCIQKEMT-PDSIRATNLHSLLVCSSAKHKM--ELLP 576
                                                                                                                                                                                              DQLRMLRVLDLEDVTFLITQKDFDRIALLCHLKYLSIGYSSSIYSLPRSIGKLQGLQTLN 558
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                                                                                                                                                                                                                                                                                                                                              148 ITVSQSFHRIELLKDMIRQLLGPSSLDQLLQELQGKVVVQVHHLSEYLIEELKEKRYFVV 207
                                                                                                                                                                                                                                                             559 MPSTYIAALPSEISKLOCLHTLRCSRKFVSDNFSLNHPMKCITNTICLPKVFTPLVSRDD 618
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 HLPSELEINPSLEALRRMVTLGYNHLPSHLKPCFLYLSIFPEDFEIKRNRLVGRWIAEGF 384
                                                                                                                                                                                                                   -SLNLLRALDLEDSSI ---SKLPDCLVTWFNLKYLNLS-KTQVKELPKNFHKLVNLETLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HLPRLKEISLGYES-----KVAGLAQLEGEVRTHPNHPVLRKREDRSDH 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             632 TKHSKIEELPLGMWKLKKLRYLITPRR-------
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Patent No. 6262343
GENERAL INFORMATION:
TITLE OF INVENTION: B62 Resistance Gene
FILE REPERENCE: 50687
CURRENT APPLICATION NUMBER: US/09/360,186
CURRENT PILING DATE: 1999-07-23
EARLIER APPLICATION NUMBER: 60/093,957
BARLIER FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 9
SEQ ID NO 3
SEQ ID NO 3
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ORGANISM: Capsicum annuum
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Best Local S
Matches 218
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A GENE FAMILY FROM THE 12 FUSARIUM RESISTANCE
LOCUS OF TOMATO AND USE THEREOF FOR TRANSFORMATION AND
SELECTIVE BREEDING OF TOMATO AND RELATED PLANTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTLAKAVY-NDESVKNHFDLKAMFCVSEAYNAFRITKGLLQEIGSIDLVDDNLNQLQVK- 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLAEKCATASLVYHLDFLQMNDAITLLLRKTNKNHEDMESNKNMQKMVERIVNKCGRLPL 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 VVQVHHLSEYLIBELKEKRYFVVLDDLW--ILHDWNWINEIAFPKNNKKGSQIVITTWNV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1240;
                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
10.9%; Score 561; DB 3; L.
Best Local Similarity 23.2%; Pred. No. 2e-45;
Matches 235; Conservative 170; Mismatches 335;
                                                                                                                                                                                                                Suite 300
                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,996A
FILING DATE: 09-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05272
FILING DATE: 15-APR-1996
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X
                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IL 113,373
                                                                                                                                                                                            ADDRESSEE: BROWDY AND NEIMARK STREET: 419 Seventh Street, N. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 13-APR-1995
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1240 amino acids
                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                             APPLICANT: ORI, Naomi
APPLICANT: PARAN, Ilan
APPLICANT: ZAMIR, Daniel
                                                                                                           TITLE OF INVENTION: A GG
TITLE OF INVENTION: LOCT
TITLE OF INVENTION: SELI
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                 GENERAL INFORMATION:
                                                                                                                                                                                                                                     D.C.
USA
                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
 Patent No. 6100449
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                              APPLICANT:
APPLICANT:
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                                                                                                                                               LVGFSDSKKRLLEMIDTNANDGPAKVICVVGMGGLGKTALSRKIFESEEDIRKNFPCNAW 147
                                                                                                                                                                  FINAL ----NDIVLDVSYPECSYLCMYKMQPFKRVTGDEINYCPYGLYRALLTPVNRQLRD 546
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                                                                                                                                                                                                                                                                                  LDDLWILHDWNWINEIAFPKNNKKGSQIVITTWNVDLAEKCATASLVYHLDFLOMNDAIT 267
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                                                                                                                  Gaps
                                                                              Query Match 11.2%; Score 576; DB 4; Length 905; Best Local Similarity 24.6%; Pred. No. 3.7e-47; Matches 218; Conservative 172; Mismatches 310; Indels 186;
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US-08-930-996A-4
; Sequence 4, Application US/08930996A
                                Capsicum annuum
               ; TYPE: PRT
; ORGANISM: Ca
US-09-864-680A-3
LENGIH: 905
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| Oy 108 DGP-AKVICVVGMGGLGKTALSRKIFESE-EDIRKNFPCNAWITVSQSFHRIELLKDMIR 165 | Db 225 GEPKLKVASIVGSGGVGKTTLATBFYRLHGRRLDAPFDCRAFVRTPRKPDMTKILTDMLS 284 | Oy 166 OLLGPSSLDQLLQBLQGKVVVQVHHLSBYLIBELKEKRYFVVLDDLWILHDWNWINEIAF 225 | DD 285 QLRPQHQASSDVWEVDRLLETIRTHLQDKRYFILIEDLWASSMWDIVSR-GL 336         | Qy 226 PKNNKKGSQIVITTWNVDLAEKCATASLVYHLDFLQMNDAITLLLRKTNKNHEDMESNKN 285 | Db 337 PDNN-SCSRILITTEIEPVALACGYNSEHIKIDPLGDDVSSQLFFSGVVGQGNEFPGH 395 | Qy 286 MQKMYUBRIVNKCGRLPLAILTIGAVLATKQVSEWEKFYEHLPSELEINPSLEALR 340   : : : | 341 RMVTLGYNHLPSHIKRPCPLYLSIFPEDFEIKRNRLVGRWIAEGFVRPKVGMTTKDVGESY | 455                                                         | Qy 401 FNELINRSMIQRSRVGIAGKIKTCRIHDIIRDITVSISRQENF-VLLPMGDGSDLVQENT 459 | DD 515 FDELVGRGIVQPVDVNCKNEVLSCVVHHMVLNFIRCKSIEENFSITLDHSQTTVRHADKV 574 | 460 RHIAFHGSMSCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVL             | 575 RRLSLHFSNAHDTTPLAGLRLSQVRSMAFFGQVKCMPSIADYRLLRVLILCFW | Qy 508 -DLEDVIFLITQKDFDRIALLCHLKYLSIGYSSSIYSLPRSIGKLQGLQTLNMPSTYIAA 566 | 567 LPSEISKLOCHTLRCSRKEVSDNFSLNHPMKCITNTICLPKVFTPLVSRDDRAIOIAEL | 682 L-LDIVHTQCLLHLRLVLLDLLPHCHRYIFT       |                                                                     | Db 712SIPKWTGKLNNLRILN-IAVMQISQDDLDTLKGLGSLTALSLLVRT 756 | Qy 687 STKEKCKILCAAIEKLSSLQY-LYVNAAGISDGGTLECLDSISSPPLLRTLVLYGSLEE 745 : : :                    | OY 746 MPNWIEQLTHLKKIYLL 762 | DD 806 FKQYDSKETGLEHLVAL 822                                                                                                                          | RESULT 7                                                                  | US-08-930-996A-2; Sequence 2, Application US/08930996A                | ; Pacent No. blod449<br>; General INFORMATION:<br>; APPLICANT: FLUHR. Robert | ESHED,<br>ORI, Na | Ilan<br>Daniel                     | ; TITLE OF INVENTION: A GENE FAMILY FROM THE 12 FUSARIUM RESISTANCE<br>; TITLE OF INVENTION: LOCUS OF TOWATO AND USE THEREOF FOR TRANSFORMATION AND | ENTION:<br>DUENCES:<br>CE ADDRES                                                                                                                                    | ; STREET: 419 Seventh Street, N.W., Suite 300                  | 2                | ; ZIP: 20004<br>; COMPUTER READABLE FORM:<br>; MEDIUM TYPE: Florov disk                                                     | Iddor |
|-------------------------------------------------------------------------|-------------------------------------------------------------------------|-------------------------------------------------------------------------|-------------------------------------------------------------------------|-------------------------------------------------------------------------|-----------------------------------------------------------------------|-----------------------------------------------------------------------------|-------------------------------------------------------------------|-------------------------------------------------------------|-------------------------------------------------------------------------|-------------------------------------------------------------------------|------------------------------------------------------------------|-----------------------------------------------------------|-------------------------------------------------------------------------|-----------------------------------------------------------------|-------------------------------------------|---------------------------------------------------------------------|----------------------------------------------------------|-------------------------------------------------------------------------------------------------|------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------|-----------------------------------------------------------------------|------------------------------------------------------------------------------|-------------------|------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------|------------------|-----------------------------------------------------------------------------------------------------------------------------|-------|
|                                                                         | IYSLPRSIGKLQGLQTLNMPSTYIAALPS                                           | Db 599 KLKLERFLDIS-RTNIKRLPDSICVLYNLETLLLSSCKLEELPLQMEKLINLR 650        | QY 586 FVSDNFSLNHPMKCITNTICLPKVFTPLVSRDDRAIQIAELHMATKSCWYKSFGVKVPKG 645 | Db 651HKDUSNIWHHKMPLH 665                                               | 646                                                                   | .XSLQVLVGAKFLVGVWR                                                          | 721 EKMHVEQLSLEWSESISADNSQTERDILDELRPHKNIQEVKIIGFRGTN             | OY 747 -PNWIEQLTHLKKIYLLRSKLKEGKTWLILGALPNLMVLDLYRKAYLG 793 | Db 770 PPNWVADPLFLKLVKLSLRNCKDCYSLPALGQLPCLKFLSVKGMHGIRVVTEEFYGRLSS 829 | Qy 794EKLVPKTGAFPNLRTLSI                                                | 830 KKPFNCLEKLEFEDMTEWKQWHALGIGEFPTLEKLSIINCPELSLEIFIQFSSLKRFRVF | 812YD                                                     | Db 890 GCPVVFYDAQVLRSQLBGMKQIBEIYIRDCNSVTSFPFSILPTTLKTIDISGCPKL-KLE 948 | 949 APVČEMSMPLEEFSVERGGYSPEFLPTAREIRRIGHTPTATETHIR              | 885 KREDRSDHDLACDAEGSPVEVEATDPLPEQEGE 917 | DD 1003 NCENVEKLSMACGGAAQLTSLDISGCKKIKCLPELLPSLKELQLTN-CPRIEGB 1055 |                                                          | RESULT 6<br>82-09-36-946B-4<br>; Sequence 4, Application US/09336946B<br>; Patent No. 06479731. | RMATIO<br>Valent             | ; APPLICANT: BYDAN GROOT A APPLICANT: B. I. du Pont de Nemours and Company ; TITLE OF INVENTION: A Pi-ta GENE CONFERRING DISEASE RESISTANCE TO PLANTS | ; FILE REFERENCE: BB-1136<br>: CURRENT APPLICATION NUMBER: US/09/336.946B | CURRENT FILING DATE: 1999-06-21 ; PRICA APPLICATION NUMBER: 60/095229 | ; FKIOK FILING DATE: 1998-08-04<br>; NUMBER OF SEQ ID NOS: 19                | ; SEQ 1D NO 4     | TYPE: PRT ; ORGANISM: Oryza sativa | B-4                                                                                                                                                 | Query Match 10.5%; Score 540; DB 4; Length 928; Best Local Similarity 25.8%; Pred. No. 1.4e-43; Matches 206; Conservative 143; Mismatches 312; Indels 136; Gaps 29; | QY 9 ARSLVGSAISKAASAAADETSLLLGVEKDIWYLFRHGVGRSNGGPVVGMVASGN 62 | AIRQESYHLGRRTSSS | Qy 63 QSCLAIDSYAEDIRNQSARNVDEAELVGFSDSKKRLLEMIDTNAN 107<br>Db 171 RPREYDDDDREDSAGNERRRFLSLTFGWDDAAVHGOLVGRDISWCKLVRRLAD 224 |       |

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346 LITTEIBPVALACCGYNSEHIIKIDPLGDDVSSQLFFSGVVGQGNEFPGHLTEVSHDMIK 405
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                                                                    861
                                                                                                                 842 FNSLVKLRFEDMPEWKQWHTLGIGEFPTLEKLSIKNC-------PELSLEIP 886
                                                                                                                                                              862 SKVAGLAQLEGEVRTHPNHPVLRKREDRSDHDLACDAEGSPVEVEATDPLPEQEGESSQR 921
                                                                                                                                                                                                                                                                                   -- KSVTSFPFSILPTTLKRIKISGCPKLKLEAPVGEMFVEYLSVIDCGCVDDISPEFLPT 958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Valent, Barbara S.
APPLICANT: Valent, Bryan, Gregory
APPLICANT: Bryan, Gregory
APPLICANT: Bryan, Gregory
APPLICANT: E. T. du Pont de Nemours and Company
TITLE OF INVENTION: A Pi-ta GENE CONFERRING DISEASE RESISTANCE TO PLANTS
FILE REFERENCE: BB-1136
CURRENT APPLICATION NUMBER: US/09/336,946B
CURRENT FILING DATE: 1999-06-21
PRIOR PLILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Microsoft Office 97
                                                                    -GSSPQLEKIEIRFCRLESGIIGIIHLPRLKEISLGYE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.5%; Score 539.5; DB 4; Length 928; 26.7%; Pred. No. 1.6e-43;
                                                                                                                                                                                                                                                         922 RDKHSSSWFYQVMISS--SIGISGRPCF------
                                                                                                                                                                                                                                                                                                                                                962 LRRLPLSSIASHALDSSLSGMNCFNLTFSRDMLLVP 997
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                                                                                                                                                                                                           887 IQFSSLKRLD------
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; Patent No. 6479731
; GENERAL INFORMATION:
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ORGANISM: Oryza sativa
                                                                       LDQLREIRFED-
                                                                                                                                                                                                                                                                                                                                                                                             959 ARQLSIE--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 VVV--QVHHLSEYLIEELKEKRYFVVLDDLW--ILHDWNWINEIAFPKNNKKGSQIVITT 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   324 RKESVALMMDSGAI--YMGILSSEDS-WALFKRHSLEHKDPKEHPEFEEVGKQIADKCKG 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 WNVDLAEKCATASLVYHLDFLQMNDAITLLLRKTINKNHEDMESNKNMQKMVERIVNKCGR 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPLAILTIGAVLATK-QVSEWEKFYEHLPSEL-EINPSLEALRRMVTLGYNHLPSHLKPC 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    381 LPLALKALAGMLRSKSEVDEWRNI---LRSEIWELPSCSNGILPALMLSYNDLPAHLKQC 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     358 PLYLSIFPEDFEIKRNRLVGRWIAEGFVRPKVGMTTKDVGESYFNELINRSMIQRSRVGI 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGKIKTCRIHDIIRDITVSISRQENFVLLPMGDGSDLVQENTRHIAFHGSMSCKTGLDWS 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        492 ERDVEEFLMHDLVNDL-AQIASSNHCIRLEDNKGSHML-EQCRH-----MSYSIGQDGE 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --PKSLAHAVCPDQLRMLRVLDLEDVTFLITQK 519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FGVKVPKGIGKLRDLQVLEYVDIRRTSSRAIKE---LGQLSKLRKLGVMTNGSTKEKCKI 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           695 LCAAIEKLSSLQYLYVNAAGISDGGTLECLDSISSPPPLLRTLVLYGSL-EEMPNWIEQL 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------DILDEL-RPHKNIKAVEITGYRGTNFPNWVADP 786
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10.5%; Score 540; DB 3; Length 1220;
Best Local Similarity 22.9%; Pred. No. 2.3e-43;
Matches 228; Conservative 170; Mismatches 360; Indels 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1220;
  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,996A
FILING DATE: 09-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05272
FILING DATE: 15-APR-1996
PRIOR APPLICATION DATA: 13-APR-1996
PRIOR APPLICATION NUMBER: IL 113,373
FILING DATE: 13-APR-1995
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                           1220 amino acids
                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                     amino acid
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697 AAIEKLSSLQY-LYVNAAGISDGGTLECLDSISSPPPLLRTLVLYGSLEEMPNWIEQLTH 755
                                                                                                                                                                                                                                        517 TOKOPORIALLCHLKYLSIGYSSSIYSLPRSIGKLOGLOTLNMPSTYIAALPSEISKLOC 576
                                                                                                                                                                                                                                                                             ---bltsipellolrylkitchitv-klpekioglohlotieadaratavi-ldivhtoc 690
                                                                                                                                                                                                                                                                                                                      577 LHTLRCSRKFVSDNFSLNHPMKCITNTICLPKVFTPLVSRDDRAIQIAELHMATKSCWYK 636
                                                                                                                                                                                                                                                                                                                                                             711
                                                                                                                                                                                                                                                                                                                                                                                                  637 SPGVKVPKGIGKLRDLQVLEYVDIRRISSRAIKELGQLSKLRKLGVMTNGSTKEKCKILC 696
                                                                                                                                                          CKT----GLDWSIIRSLAIFGDRPKSLAHAVCPDQL---RMLRVL-----DLEDVTFLI 516
                                                                                                                                                                                                                                                                                                                                                       LIHIRI---VILD--LIPH------CHRYIFT-------
                                                                              QRSRVGIAGKIKTCRIHDIIRDITVSISRQENF-VLLPMGDGSDLVQENTRHIAFHGSMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Staskawicz, Brian S., Oldroyd, Giles Edward, APPLICANT: Stancron, John M., Rommens, Caius TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PLANT TITLE OF INVENTION: PATHOGEN RESISTANCE OF RESOURCES: 15 CORRESPONDENCE ADDRESS: ADDRESSEE: Klarquist Sparkman Campbell Leigh & ADDRESSEE: Whinston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 35,123
REFERENCE/DOCKET NUMBER: 5151-45038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/680,327
FILING DATE: July 11, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/310,912
FILING DATE: September 22, 1994
CLASSIFICATION: 800
APPLICATION: WUMBER: 08/227,360
FILING DATE: April 13, 1994
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      One World Trade Center
121 S.W. Salmon Street
Suite 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08680327; Patent No. 5859321; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM FC COMPALIBLE
OPERATING SYSTEM: MS DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Alan. E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               756 LKKIYLL 762
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STREET:
STREET:
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                                                                                                                                                                                                           AANEGFGSLKYFMFV-----CTAPCMTFVEGAMPSVQRLNLRFNANEFKQYDSKETG 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EDIRNQSARN------VDEA----ELVGFSDSKKRLLEMIDTNANDGP-AKVICV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 VGMGGLGKTALSRKIFESE-EDIRKNFPCNAWITVSQSFHRIELLKDMIRQLLGPSSLDQ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 LLQELQGKVVVQVHHLSEYLIEELKEKRYFVVLDDLWILHDWNWINBIAFPKNNKKGSQI 235
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                                                                                                                                                                                LHTLRCSRKFVSDNFSLNHPMKCITNTICLPKVFTPLVSRDDRAIQIAELHMATKSCWYK 636
                                                                                                                                                                                                                                                             637 SFGVKVPKGIGKLRDLQVLEYVDIRRTSSRAIKELGQLSKLRKLGVMTNGSTKEKCKILC 696
                                                                                                                                                                                                                                                                                   AAIEKLSSLQY-LYVNAAGISDGGTLECLDSISSPPPLLRTLVLYGSLEEMPNWIEQLTH 755
                                                                                                    TOKOPDRIALLCHLKYLSIGYSSSIYSLPRSIGKLOGLLNMPSTYIAALPSBISKLOC
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APPLICANT: Valent, Barbara
APPLICANT: Bryan, Gregory
TITLE OF INVENTION: Modification of a Plant Disease Resistance Gene
TITLE OF INVENTION: Specificity and Method for Engineering Altered
TITLE OF INVENTION: Specificity
FILE REFERENCE: BB1385 US NA
CURRENT APPLICATION NUMBER: 08/09/993,170
CURRENT FILING DATE: 2010-11-26
PRIOR APPLICATION NUMBER: 60/248,335
PRIOR FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Microsoft Office 97
SEQ ID NO 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.5%; Score 539.5; DB 4; Length 928; 26.7%; Pred. No. 1.6e-43;
                    CKT----GLDWSIIRSLAIFGDRPKSLAHAVCPDQL---RMLRVL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 58, Application US/09993170
; Patent No. 6743969
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                     LKKIYLL 762
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LEHLVAL 822
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US-09-993-170-58
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                                                                                                                                                                    -LLQINSGEGVFPERLEEYRLFVH---SYQDEIDLWRPSRSNVRSL-----LFNAI 1478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87 ELVGFSDSKKRLLEMIDTNANDGP-AKVICVVGMGGLGKTALSRKIFESEEDIRKNFPCN 145
                                                                                                                                                                                                  146 AWITVSQSFHRIELLKDMIRQLLGPSSLDQLLQELQGKVVVQVHHLSEYLIEELKEKRYF 205
                                                                                                                                                                                                                                             VVLDDLWILHDWNWINEIAFPKNNKKGSQIVITTWNVDLAEKCATASLVYHLDFLQMNDA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CPDQL------RMLRVLDLEDVTFLITQKDFDRIALLCHLKYLSIGYSSSIYS 543
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                                                                                                                                                                                                                                                                                       ITLLLRKTNKNHEDMESNKNMQKMVERIVNKCGRLPLAILTIGAVLATKQ--VSEWEKFY 323
                                                                                                                                                                                                                                                                                                                                                                            FVRPKVGMTTKDVGESYFNELINRSMIQRSRVGIAGKIKTCRIHDIIRDITVSISRQENF 443
                                                                                                                                                                                                                                                                                                                                                                                                                      VLLPMGDGSDLVQENTR--HIAFHGSMSCKTGLD-W----SIIRSLAIFGDRPKSLAHAV 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             544 LPRSIGKLQGLQT-----LUNMPSTYIAALPSEISKLQCLHTLRCSRKFVSD--NFS 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LNHPMKCITNTICLPKVFTPLVSRDDRAIQIAELHMATKSCWYKSFGVKVPKGIGKLRDL 652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TML-ILGALPNLMVLDLYRKAYLGEKLVFKTGAFPNLRTLSIYDLDQLREIRF--EDGSS 827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LHENMDVLTGNSQLPNLET-----GK----
                                                                                                                                   Gaps
                                                                                                             Query Match
10.3%; Score 530; DB 2; Length 1824;
Best Local Similarity 24.9%; Pred. No. 4.5e-42;
Matches 201; Conservative 154; Mismatches 279; Indels 172;
                                                                                                           Length 1824
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PKLEHLVLTKCK-----HLEKI 1765
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 228-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
; LENGTH: 1824 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-680-327-3
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RESULT 11 US-09-228-246-2

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1432 -LLQINSGEGVFPERLEEYRLFVH---SYQDEIDLWRPSRSNVRSL------LFNAI 1478
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                                                                                                  Compositions
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                    patent No. 6245510
GENERAL INPORMATION:
APPLICANT: Staskawicz, B. S. et al.
APPLICANT: Staskawicz, B. S. et al.
TITLE OF INVENTION: PRF Protein and Nucleic Acid Sequences: Compc;
TITLE OF INVENTION: and Methods for Plant Pathogen Resistance
FILE REFERENCE: 51700
CURRENT APPLICATION NUMBER: US/09/228,246
CURRENT APPLICATION NUMBER: 08/680,327
EARLIER APPLICATION NUMBER: 08/680,327
EARLIER PILING DATE: 1996-09-11
EARLIER FILING DATE: 1996-09-11
EARLIER FILING DATE: 1994-09-22
EARLIER FILING DATE: 1994-09-22
SAFILIER FILING DATE: 1994-04-13
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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Sequence 2, Application US/09228246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) ORGANISM: Lycopersicon esculentum
US-09-228-246-2
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Best Local Similarity
Matches 201; Conserv
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1048 VGFDRVDVLSRRCPN------LQQLQITYFGNNEP---FCPKLENLTQLQQLQL 1093
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                                                                                                                                                                                                                                                          1124 -IPFIAGLPSLEYLOLODVCFPQSBEWCLGDITFHKLKLKLIKLVKLNISRWDVSEE-SFPL 1181
                                                             ---EYVDI--RRISSRAIKELGQLSKLRKLGVMTNGSTKEKCKILCAAIEKLSSLQYLYV 710
                                                                                                                                         NAAGISDGGTLECLDSISSPPPLLRTLVLYGSLEEMPNWIEQLTHLKKIYLLRSKLKEGK 770
                                                                                                                                                                                                                     771 TMLILGALPNLMVLDLYRKAY-LGEKLVFKTGAFPNLRTLSIYDLDQLREIRFEDGSSPQ 829
                                                                                                                                                                                                                                                                                                830 LEKIEIRFC-RLESGIIGIIHLPRLKEISLGYESKVA---GLAQLEGEVRTHPNHPVLRK 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Michelmore, Richard W. APPLICANT: Shen, Kathy APPLICANT: Meyers, Blake TITLE OF INVENTION: Procedures and Materials for TITLE OF INVENTION: Conferring Pest Resistance in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,838
FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "RLG1A amino acids"
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                      ------DXQCIDS-----
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CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/781,734
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 11, Application US/09004838; Patent No. 6350933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 023
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 1402 amino acids
amino acid
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend
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LOCATION: 1..1402
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   1242 VKQRSD 1247
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                                                                 -----LESLKLVSNSYP-----AKLPHKFNFPSQLRELTL--SKFRLPW 1691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    542 YSLPRSIGKLQGLQTLNMPSTYIAALPS---EISKLQCLHTLRCSRKFVSDNFSLNHPMK 598
                                           TML-ILGALPNLMVLDLYRKAYLGEKLVFKTGAFPNLRTLSIYDLDQLREIRF--EDGSS 827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VDEAELVGFSDSKKRLLEMIDTNANDGPAKVICVVGMGGLGKTALSRKIFESEEDIRKNF 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 PCNAWITVSQSFHRIELLKDMIRQLLGPSSLDQLLQELQGKVVVQVHHLSEYLIEELKEK 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RYFVVLDDLWILHDWNWINBIAFPKNNKKGSQIVITTWNVDLAEKCATASLVYHLDFLQM 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263 NDAITLLLRKTNKNHEDMESNKNMOKMVERIVNKCGRLPLAILTIGAVLATKQVSE--W- 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   693 EESCQLLOKKV---FQKEDCPPELODVSQAVAEKCKGLPLVVVLVAGIIKKRKMEESWWN 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---EKFYEHLPSELEINPSLEALRRWYTLGYNHLPSHLKPCFLYLSIFPEDFEIKRNRLV 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  435 VSISRQENFVLLPMGD------GSDLVQENTRHIAFHGSMSCKTGLDW-SIIRSLA 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Tankeley, Steven D.
APPLICANT: Tankeley, Steven D.
APPLICANT: Brommonschenkel, Sergio H.
TITLE OF INVENTION PLANT GENE CONFERRING RESISTANCE TO TOSPOVIRUSES FILE REFERENCE: 19603/3201
CURRENT APPLICATION NUMBER: US/09/803,286A
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 60/188,356
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tch 10.2%; Score 525; DB 4; Length 1247; al Similarity 24.3%; Pred. No. 7.2e-42; 206; Conservative 158; Mismatches 318; Indels 164;
                                                                                                                                               828 PQLEKIEIRFCRLESGIIGIIHLPRL 853
                                                                                                                                                                                                                                                       Sequence 2, Application US/09803286A Patent No. 6664447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Lycopersicon var.
US-09-803-286A-2
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                                                                                              MVASGNQSCLAIDSYAE-DIRNQSARNVDEAELVGFSDSKKRLLEMIDTNANDGPAK--- 112
                                                                                                                              VICVVGMGGLGKTALSRKIPESEEDIRKNFPCNAMITVSQSFHRIELLKDMIRQLLGPSS 172
                                                                                                                                                                                                                    -----LSYNDLSAXLKILLPAYCSLPPKDYEFDKEELILLWMAEGFLHQPTXNKSKQRLG 829
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                                               Indels 307;
Length 1402;
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10.0%; Score 512.5; DB 3; llarity 23.2%; Pred. No. 1.5e-40; Conservative 154; Mismatches 307;
                      al Similarity
232; Conserv
  Query Match
Best Local S
Matches 232
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387 PKVGMTTKDVGESYFNELINRSMIQRSRVGIAGKIKTCRIHDIIRDITVSISRQEN-FVL 445
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OTHER INFORMATION: Description of Artificial Sequence: ORF2 encoded
OTHER INFORMATION: polypeptide
                                                                                             TITLE OF INVENTION: RESISTANCE AGAINST NEMATODES AND/OR APHIDS FILE REFERENCE: 960-35
CURRENT APPLICATION NUMBER: US/09/245,928A
CURRENT APPLICATION NUMBER: US/09/246,928A
CURRENT FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: PCT/EP97/04340
PRIOR APPLICATION NUMBER: EP96401764.4
PRIOR APPLICATION NUMBER: EP97401101.7
PRIOR FILING DATE: 1996-08-09
PRIOR PILING DATE: 1996-06-16
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATEILING VOS: 19
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; Sequence 19, Application US/09245928A
; Patent No. 6613962
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                                                    GENERAL INFORMATION:
APPLICANT: KEYGENE N.V.
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Matches 235;
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| :: :                                             | 269                                     | Oy 327 PSELEINPSLEALRRWYT   : :   :   : :::   330 SSF1-LINSEVEWW-KVIE   387 PKVGMTTKDVGESYFNEL   387 PKVGMTTKDVGESYFNEL | 8 4 4 6 6 6                                                    | Oy 495 AVCPDQLRMLRVLDLEDV                                                                                                                                                                                                                 | Oy 615 SRDDRAIQIAELHWATKS  Db 983  Qy 673 OLSKLRKLGVWTNGSTKE  Db 1013 KLENLRILGELLISYSKD  OY 711 NAAGISDGGTLECLDSIS  Db 1073 LCVGFKSSNTNHCGSSVA  OY 764 SKLKEGKTWLILGALPNL  Db 1124                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
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| Db 910:-RTOVKXLPFSF8NLWNLESLFVSNKGSILVLLPRIL 945 | KVPKGIGKLRDLQVLEYVDIRRTSSRAIKELG 67<br> |                                                                                                                         | 764 SKLKEGKTWLILGALPNLMVLDLYRKAYLGEKLVFKTGAFPNLRTLSIYDLDQL<br> | Qy         818 REIRFEDGSSPQLEKIEIRFC-RLESGIIGIIHLPRLKEISL 858           Db         1127SKWEVGEESFPNLEKLKLQECGKLEEIPPSFGDIYSLKFIKIVKSPQLEDSALKIKKY 1184           Qy         859GYESKVAG 866           Db         1185 AEDMRGGNELQILG 1198 | RESULT 15  US-02-245-28A-17  Sequence 17, Application US/09245928A  Faren No. 6613962  GENERAL INPORMATION:  PAPLICANTON WESESTANCE AGAINST NEMATODES AND/OR APHIDS  TITLE OF INVENTION:  TITLE OF INVENTION:  TITLE OF INVENTION WHORE: 1997-08-08  FRICK PILLEM DATE: 1997-08-08  FRICK PILLEM DATE: 1997-08-08  FRICK PILLEM DATE: 1997-08-08  FRICK PILLEM DATE: 1997-08-08  FRICK PILLEM DATE: 1997-08-08  FRICK PILLEM DATE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHORE: 1997-08-08-08  FRICK APPLICATION WHORE: 1997-08-08  FRICK APPLICATION WHO |

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Sequence 104966,
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Copyright (c) 1993 - 2005 Compugen Ltd
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US-10-437-963-110261
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Publication No. US20040006788A1
Publication No. US20040006788A1
Fublication No. US20040006788A1
Fub. GENERAL INFORMATION:
APPLICANT: Liu, Guifu
TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in PlacTHER REFERENCE: 22727/04108
CURRENT APPLICATION NUMBER: US/10/352,179
CURRENT FILING DATE: 2003-01-27
RECORD FILING DATE: 2002-01-25
NUMBER OF SEQ 1D NOS: 97
SOFTWARE: Patentin version 3.1
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; ORGANISM: Oryza minuta
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81.2%; Score 4169.5;
Best Local Similarity 79.0%; Pred. No. 0;
Matches 848; Conservative 21; Mismatches
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                       TYPE: PRT
ORGANISM: Oryza
SEQ ID NO 93
LENGTH: 1091
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APPLICANT: Wang, Guo-liang
APPLICANT: Liu, Guifu
TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in FILE REFERENCE: 22727/04108
CURRENT APPLICATION NUMBER: US/10/352,179
PRIOR APPLICATION NUMBER: 60/352,106
PRIOR APPLICATION NUMBER: 60/352,106
PRIOR FILING DATE: 2002-01-25
SOFTWARE: Patentin version 3.1
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              TNANDGPAKVICVVGMGGLGKTALSRKIFESEEDIRKNFPCNAWITVSQSFHRIELLKDM
                                                                                                                           AFPKNNKKGSRIVITTRNVDLAEKCATASLVYHLDFLQMNDAITLLLKRTINKNHEDMESN
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                            TNANDGPAKVICVVGMGGLGKTALSRKIFBSBEDIRKNPPCIAWITVSQSFHRIBLLKDM
                                                                          KNMQKOMVERIVNKCGRLPLAILTIGAVLATKHVSEWEKFYEQLPSELEINPSLEALRRMV
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Publication No. US20040006788A1
GENERAL INFORMATION:
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US-10-352-179-93
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APPLICANT: LA ROSA, Thomas J.
APPLICANT: LA ROSA, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Yahua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Buukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plante and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (5321) B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
KUMBER OF SEQ ID NOS: 204966
SEQ ID NO 104966
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_102251C.1.pep
US-10-437-963-104966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 104966, Application US/10437963; Publication No. US20040123343A1; GENERAL INFORMATION:
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; Sequence 139799, Application US/10437963
; Publication No. US20040123343A1
; Publication No. US20040123343A1
; Bublication No. US20040123343A1
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Bukharov, Andrey A.
; APPLICANT: Bukharov, Andrey A.
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Dlants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT APPLICATION NUMBER: US/10/437,963
; SEQ ID NO 139799
; LENTH: 1531
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US-10-437-963-139799
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89.3%; Pred. No. 0;
tive 17; Mismatches
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817; Conservative
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                                                                                                                                51.0%; Score 2621; DB 15;
llarity 55.3%; Pred. No. 4.6e-210;
Conservative 134; Mismatches 217;
 NUMBER OF SEQ ID NOS: 97
SOFTWARE: Patentin version 3.1
SEQ ID NO 85
LENGTH: 979
                                                                                ; ORGANISM: Oryza minuta
US-10-352-179-85
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                                                  TNANDGPAKVICVVGMGGLGKTALSRKIFESEEDIRKNFPCNAWITVSOSFHRIELLKDM
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APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 141086
LENGTH: 862
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Publication No. US20040123343A1;
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei;
APPLICANT: Cao, Yongwei;
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
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ORGANISM: Oryza sativa
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APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Buchharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ring
TITLE OF INVENTION: Plante and Uses Thereof for Plant Improvement
FILE OF INVENTION: Plantes and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53221)B
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 143499
LENGTH: 974
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VASGNOSCLAI------DSYAEDIRNOSARNVDEAELVGPSDSKKRLLEMIDTN 105
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US-10-437-963-143499
                                                                                                                                                                         Sequence 143499, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
                                                                                                                                                                                                                          APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Bukharov, Andrey A.
APPLICANT: Barbaruk, Brad
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Best Local Similarity
Matches 539; Conserv
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Barbazuk, Brad
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ORGANISM: Oryza sativa
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Best Local Similarity
Matches 488; Conserv
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
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With
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated I
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 110261
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US-10-437-963-110261
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llarity 48.2%; Pred. No. 2.1e-173;
Conservative 143; Mismatches 279;
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APPLICANT: La Rose, Thomas J.
APPLICANT: La Rose, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwel
APPLICANT: Wu, Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Brice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NOS: 204966
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 GRPNSGDFNLNDPKDCLIAFSCLPLLMAATDS-DERNKIIAELHVGCSSQWSPNGGTYGV
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US-10-437-963-151916
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41.0%; Score 2105; DB 16;
Best Local Similarity 52.2%; Pred. No. 1.1e-166;
Matches 448; Conservative 143; Mismatches 247;
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ORGANISM: Oryza sativa
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APPLICANT: Wang, Guo-liang
APPLICANT: Liu, Guifu
TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pla
FILE REFENCE: 22727/04108
CURRENT APPLICATION NUMBER: US/10/352,179
CURRENT FILING DATE: 2003-01-27
PRIOR PRILING DATE: 2002-01-25
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn version 3.1
                                                                                                                                      950
                                             754 THLKKIYLLRSKLKEGKTMLILGALPNLMVLDLYRKAYLGEKLVFKTGAPPNLRTLSIYD 813
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                                                                                                                        VRTHPNHPVLRKREDRSDHDLACDA----EGSPVEVEATDPLPEQEGESSQ 920
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                                                                                                                                                                                                                                                                      ; Sequence 87, Application US/10352179; Publication No. US20040006788A1; GENERAL INFORMATION:
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ORGANISM: Oryza minuta
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478; Conservat
                                                                                                                                                                                                                                                           US-10-352-179-87
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                                                                                                                                   ------PVVGM 57
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                                                                                                     QLLGPSSLDQLLQELQGKVVVQVHHLSEYLIEELKEKRYFVVLDDLWILHDWNWINBIAF
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                                                                                        1 MAETVLSMARSLVGSAISKAASAAADETSLLLGVEKDIWYL
                                            1 Similarity 45.9%; Score 2103.5; DB 15 Similarity 45.9%; Pred. No. 1.2e-166; 10; Conservative 131; Mismatches 244;
             Oryza minuta
                                           Query Match
Best Local Simi:
Matches 480;
    ; TYPE: FK:
; ORGANISM: Or
US-10-352-179-91
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AHAVCPDQLRMLRVLDLEDVTFLITQKDFDRIALLCHLKYLSI------GYSSSIY 542
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                                              TKQVSEWEKFYEHLPSELEINPSLEALRRMVTLGYNHLPSHLKPCFLYLSIFPEDFEIKR 372
                                                                                                                                                                    NRLVGRWIAEGFVRPKVGMTTKDVGESYFNELINRSMIQRSRVGIAGKIKTCRIHDIIRD 432
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                                                                              LVYHLDFLOMNDAITLLLRKTNKNHEDMESNKNMOKMVERIVNKCGRLPLAILTIGAVLA
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Publication No. US2004006788A1
GENERAL INFORMATION:
APPLICANT: Wang, Guo-liang
APPLICANT: Liu, Guifu
TITLE OF INVENTION: Procedures and Materials for FILE OF INVENTION: Procedures and Materials for FILE OF FILE OF INVENTION: Procedures and Materials for FILE OF FILE OF INVENTION UNMBER: US/10/352,179
CURRENT FILING DATE: 2003-01-27
PRIOR APPLICATION NUMBER: 60/352,106
PRIOR FILING DATE: 2002-01-25
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn version 3.1
SEQ ID NO 91
LENGTH: 1054
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| RESULT 12 US-10-437-963-177336 Sequence 177356, Application US/10437963 Sequence 177356, Application US/10437963 Sequence 177356, Application US/10437963 GENERAL INFORMATION: APPLICANT: La Rosa, Thomas J. APPLICANT: Cao, Yongwei APPLICANT: Cao, Yongwei APPLICANT: Cao, Yongwei APPLICANT: Boukharov, Andrey A. APPLICANT: Buckharov, Andrey A. APPLICANT |                                                                                                                                                                                                                                                                                                                                                                                |
| A B B B B B B B B B B B B B B B B B B B                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | ; Publication No. US2040123343A1<br>; GENERAL INFORMATION:<br>; APPLICANT: La Rosa, Thomas J.<br>; APPLICANT: Zhou, Yihua<br>; APPLICANT: Cao, Yongwei<br>; APPLICANT: Wu, Wei<br>; APPLICANT: Boukharov, Andrey A.                                                                                                                                                            |
| QY         114 ICVVGMGGLGKTALSRKIFESEEDIRKNPPCNAMITVSQSFHRIELLKDMIRQLLGPSSL 173           Db         110 ICVVGMGGLGKTALSRKIFESEEDIRKNPPCNAMITVSQSFHRIELLKDMIRQLLGPSSL 169           QY         174 DQLLQELQGKVVVQVHHLSEYLEELKGKKFF-VVLDDLWILHDWNWINEIAFPKNNKKG 232           Db         170 DQLLQELQGKVVVQVHHLSEYLIEELKGKKRFSSVVGRLIHFHRPQQLSTVSLPLPLDPA 229                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | ; APPLICANT: Barbazuk, Brad ; APPLICANT: Li, Ping ; APPLICANT: Li, Ping ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement ; FILE REPERENCE: 38-21(53221)B ; CURRENT APPLICATION NUMBER: US/10/437,963 ; CURRENT FILING DATE: 2003-05-14 ; NUMBER OF SEQ ID NOS: 204966 |
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| 305LIIGAVLATKQVSEWEKPYEHLPSELEINPSLEALRRWTLGYNHLPSHLKP 315 1ASQLFARMSERACVHGRDIEEWEILYAQLFSELGCNFSLYABANKKVVALSYNYLPSHLKP 316 1ASQLFARMSERACVHGRDIEEWEILYAQLFSELGCNFSLAAMKKVVALSYNYLPSHVKP 317 1AGKIKTCRIHDIIRDIKANRLVGRWIAEGFVRAKGGEFWWD                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Clone ID: 30.5%; (737.0%; (737.0%; (742.041)                                                                                                                                                                                                                                                                                                                                   |

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                                                                                                       YWSAKNIDEAELVGFDDAKESILNLIDVHANHGLAKVIFVVGMGGLGKTSLVKKVYHS-I 233
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APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Fing
APPLICANT: Li, Fing
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 157799
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|033 SEERNLVLVLDEHSISSSKDKVRHLVISQSWSREQKKNNDMQNIVDVSHIRSLTVFGEW- 1091
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                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 22.8%; Score 1172; DB 16; Best Local Similarity 33.9%; Pred. No. 2.7e-88; Matches 326; Conservative 163; Mismatches 312;
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Cao, Yongwei
Wu, Wei
Boukharov, Andrey
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648 KLRDLQVLEYVDIRRTSSRAIKELGQLSKLRKLGVMTNGSTKEKCKILCAAIEKLSSLQY 707

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Sequence 157799, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.

RESULT 14 US-10-437-963-157799

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969 -----AWLRNLDVCGVKVPRGIGRLRSIHTLSIVNIAR-GKALLKNLKKLTQLCKLGV-- 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                 1021 TGINKNNCKELCSAIADHGRLQSLLLRAEG--NAGLEGCLDNMSQPPKDLKSLQLYGNLV 1078
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                                                              935 EDDQPIIKLLHQFRSIREEMGTRFAVSYIMLFIT------968
                                      SRVGIAGKIKTCRIHDIIRDITVSISRQENFVLLPMGDGSDLVQENTRHIAFHGSMSCKT 472
                                                                                                                                 820 NDMQNIVDVSHIRSLTVPGEW-KSF---FLSKKOMRMLRVLDLEDABGL-QDPDLVPIGKL 874
                                                                                                                                                                                                           MATKSCWYKSP---GVKVPKGIGKLRDLQVLEYVDIRRISSRAIKELGQLSKLRKLGVMT 684
 700 HLKSCFLYMSIFPEDSDIRYRRLLRRWTAEGYSRATRNRSNEKVAEEQFTALLNKSMIQQ 759
                                                                                                              G----LDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLEDVTFLITQKDFDRIALL 527
                                                                                                                                                                                    CHLKYLSIGYSSSIYSLPRSIGKLQGLQTLNMPSTYIAALPSEISKLQ----- 575
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Job time : 97.9347 secs
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Sequence 135087, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Brad

APPLICANT: Boukharov, Brad

APPLICANT: Boukharov, Brad

APPLICANT: Boukharov, Brad

APPLICANT: Boukharov, Brad

APPLICANT: Boukharov, Brad

APPLICANT: Boukharov, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 135087
KEGKTWLILGALPNIAVLDLYRKAYLGEKLVFKTGAFPNIRTLSIYDLDQLREIRFEDGS 826
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                                                                                                                                                                                                      SPQLEKIEIRPCRL--ESGIIGIIHLPRLKEISL-GY---ESKVAGLAQLEGEVRTHPNH 880
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_36797C.1.pep
US-10-437-963-135087
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ORGANISM: Oryza Bativa
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